



#5

## SEQUENCE LISTING

5

## (1) GENERAL INFORMATION

(i) APPLICANT: NovoNordisk, BioImage

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(ii) TITLE OF THE INVENTION: A Method of Detecting Cellular  
Translocation of Biologically Active Polypeptides Using  
Fluorescence Imaging

(iii) NUMBER OF SEQUENCES: 143

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: NovoNordisk, BioImage

(B) STREET: Mørkhøjbygade 28

(C) CITY: Søborg

(D) STATE: DK

20

(E) COUNTRY: DENMARK

(F) ZIP: 2860

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

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(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: , PV&amp;P R

(B) REGISTRATION NUMBER:

(C) REFERENCE/DOCKET NUMBER:

35

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

40

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGACACAA GCTTTGGACA CGGCGGCCCA TGAGTAAAGG AGAAGAACTT TTC

53

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

55

(D) TOPOLOGY: linear

58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTCATCTTCT CGAGTCTTAC TCCTGAGGTT TGTATAGTTC ATCCATGCCA TGT

53

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTGGACACAA GCTTTGGACA CCCTCAGGAT ATGGGCAACG CCGCCGCCGC CAAG

54

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCATCTTCT CGAGTCTTTC AGGCGCGCCC AAATCAGTA AACTCCTTGC CACAC

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTGGACACAA GCTTTGGACA CCCTCAGGAT ATGGCTGACG TTACCCGGC CAACG

55

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

50

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

55

GTCATCTTCT CGAGTCTTTC AGGCGCGCCC TACTGCACTT TGCAAGATTG GGTGC

55

58

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## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTGGACACAA GCTTTGGACA CCCTCAGGAT ATGGCGGCGG CGGCGGCGGC TCCGGGGGGC 60  
GGGG 64

15

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCATCTTCT CGAGTCTTTC AGGCGCGCCC GGGGCCCTCT GGCGCCCTG GCTGG 55

30

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

40 TAGAATTCAA CCATGGCGGC GCGGCGGCG 30

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TAGGATCCCT AGGGGGCCTC CAGCACTCC 29

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## (2) INFORMATION FOR SEQ ID NO:11:

59

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

10 TACTCGAGTA ACCATGGCGG CGGCGGCGGC G 31

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
15 (A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAGGATCCAT AGATCTGTAT CCTGG 25

25 (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TAGGATCCTT AAGATCTGTA TCCTGG 26

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
40 (A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

50 ATCTCGAGGG AAAATGTCTC AGGAGAGG 28

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
55 (A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

60



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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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ATGGATCCTC GGACTCCATC TCTTCTTG

28

(2) INFORMATION FOR SEQ ID NO:16:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGGATCCTC AGGACTCCAT CTCTTCTTG

29

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTCTCGAGCC ATCATGAGCA GAAGCAAG

28

35

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

40

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

45

GTGGATCCCA CTGCTGCACC TGTGCTA

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

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(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

61

GTGGATCCTC ACTGCTGCAC CTGTGCTA

28

(2) INFORMATION FOR SEQ ID NO:20:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

15 CGCGAATTCC GCCACCATGA GTGCTGAGGG GTACCAGTAC

40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGCGGATCCT GTCGCCTCTG CTGTGCATAT AC

32

30 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: p85-top-C

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGGAGATCTA TGAGTGCTGA GGGGTACCAG

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45 (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

50

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

55

GGGCGGATCC TCATCGCCTC TGCTGTGCAT ATAC

34

62

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTGAATTCGA CCATGTCGTC CATCTTGCCA TTC

33

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTGGTACCCA TGACATGCTT GAGCAACGCA C

31

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTGGTACCTT ATGACATGCT TGAGCAACGC AC

32

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTGAATTCGT CAATGGAGCT GGAAAACATC G

31

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

64

(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTGGATCCCT GCTGCTTCCG GTGGAGTTCG 30

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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGGATCCCT AGCTGCTTCC GGTGGAGTTC G 31

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTAGATCTAC CATGGCGGGC TGGATCCAGG CC 32

30

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTGGTACCCA TGAGAGGGAG CCTCTGGCAG A 31

40

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GTGGTACCCA TGAGAGGGAG CCTCTGGCAG A 31

50

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

5 GTGGTACCTC ATGAGAGGGA GCCTCTGGCA G 31

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTGAATTCAA CCATGGACAA TATGTCTATT ACG 33

20 (2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

30 GTGGATCCCA GTCTAAAGGT TGTGGGTCTG C 31

(2) INFORMATION FOR SEQ ID NO:35:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

45 GTGGATCCTC AGTCTAAAGG TTGTGGGTCT GC 32

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

66

GTCTCGAGGC ACCATGAGCG ACGTGGC

27

(2) INFORMATION FOR SEQ ID NO:37:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGGGATCCGA GGCCGTGCTG CTGGCCG

27

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(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1896 base pairs

20 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1891

(D) OTHER INFORMATION:

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG 48

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

35

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GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC 96

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

40

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30

GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC 144

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

35

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45

45 TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC 192

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

50

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CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG 240

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys

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CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG 288

Gln His Asp Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

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	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
5	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
10	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
15	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
20	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
25	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC	576
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
30	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG	624
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
	195 200 205	
35	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC	672
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
	210 215 220	
40	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC	720
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	
45	GGA CTC AGA TCT CGA GCT CAA GCT TCG AAT TCA ACC ATG GCG GCG GCG	768
	Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Ala Ala Ala	
	245 250 255	
50	GCG GCT CAG GGG GGC GGG GGC GGG GAG CCC CGT AGA ACC GAG GGG GTC	816
	Ala Ala Gln Gly Gly Gly Gly Gly Glu Pro Arg Arg Thr Glu Gly Val	
	260 265 270	
55	GGC CCG GGG GTC CCG GGG GAG GTG GAG ATG GTG AAG GGG CAG CCG TTC	864
	Gly Pro Gly Val Pro Gly Glu Val Glu Met Val Lys Gly Gln Pro Phe	
	275 280 285	
60	GAC GTG GGC CCG CGC TAC ACG CAG TTG CAG TAC ATC GGC GAG GGC GCG	912
	Asp Val Gly Pro Arg Tyr Thr Gln Leu Gln Tyr Ile Gly Glu Gly Ala	
	290 295 300	
65	TAC GGC ATG GTC AGC TCG GCC TAT GAC CAC GTG CGC AAG ACT CGC GTG	960
	Tyr Gly Met Val Ser Ser Ala Tyr Asp His Val Arg Lys Thr Arg Val	
	305 310 315 320	

68

	GCC ATC AAG AAG ATC AGC CCC TTC GAA CAT CAG ACC TAC TGC CAG CGC Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln Arg 325 330 335	1008
5	ACG CTC CGG GAG ATC CAG ATC CTG CTG CGC TTC CGC CAT GAG AAT GTC Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe Arg His Glu Asn Val 340 345 350	1056
10	ATC GGC ATC CGA GAC ATT CTG CGG GCG TCC ACC CTG GAA GCC ATG AGA Ile Gly Ile Arg Asp Ile Leu Arg Ala Ser Thr Leu Glu Ala Met Arg 355 360 365	1104
15	GAT GTC TAC ATT GTG CAG GAC CTG ATG GAG ACT GAC CTG TAC AAG TTG Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys Leu 370 375 380	1152
20	CTG AAA AGC CAG CAG CTG AGC AAT GAC CAT ATC TGC TAC TTC CTC TAC Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile Cys Tyr Phe Leu Tyr 385 390 395 400	1200
	CAG ATC CTG CGG GGC CTC AAG TAC ATC CAC TCC GCC AAC GTG CTC CAC Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu His 405 410 415	1248
25	CGA GAT CTA AAG CCC TCC AAC CTG CTC AGC AAC ACC ACC TGC GAC CTT Arg Asp Leu Lys Pro Ser Asn Leu Leu Ser Asn Thr Thr Cys Asp Leu 420 425 430	1296
30	AAG ATT TGT GAT TTC GGC CTG GCC CGG ATT GCC GAT CCT GAG CAT GAC Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala Asp Pro Glu His Asp 435 440 445	1344
35	CAC ACC GGC TTC CTG ACG GAG TAT GTG GCT ACG CGC TGG TAC CGG GCC His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala 450 455 460	1392
40	CCA GAG ATC ATG CTG AAC TCC AAG GGC TAT ACC AAG TCC ATC GAC ATC Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile Asp Ile 465 470 475 480	1440
	TGG TCT GTG GGC TGC ATT CTG GCT GAG ATG CTC TCT AAC CGG CCC ATC Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg Pro Ile 485 490 495	1488
45	TTC CCT GGC AAG CAC TAC CTG GAT CAG CTC AAC CAC ATT CTG GGC ATC Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu Gly Ile 500 505 510	1536
50	CTG GGC TCC CCA TCC CAG GAG GAC CTG AAT TGT ATC ATC AAC ATG AAG Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn Met Lys 515 520 525	1584
55	GCC CGA AAC TAC CTA CAG TCT CTG CCC TCC AAG ACC AAG GTG GCT TGG Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr Lys Val Ala Trp 530 535 540	1632



69

	GCC AAG CTT TTC CCC AAG TCA GAC TCC AAA GCC CTT GAC CTG CTG GAC	1680
	Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu Asp Leu Leu Asp	
	545 550 555 560	
5	CGG ATG TTA ACC TTT AAC CCC AAT AAA CGG ATC ACA GTG GAG GAA GCG	1728
	Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr Val Glu Glu Ala	
	565 570 575	
10	CTG GCT CAC CCC TAC CTG GAG CAG TAC TAT GAC CCG ACG GAT GAG CCA	1776
	Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Thr Asp Glu Pro	
	580 585 590	
15	GTG GCC GAG GAG CCC TTC ACC TTC GCC ATG GAG CTG GAT GAC CTA CCT	1824
	Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp Leu Pro	
	595 600 605	
20	AAG GAG CGG CTG AAG GAG CTC ATC TTC CAG GAG ACA GCA CGC TTC CAG	1872
	Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg Phe Gln	
	610 615 620	
25	CCC GGA GTG CTG GAG GCC C CCTAG	1896
	Pro Gly Val Leu Glu Ala Pro	
	625 630	
30	(2) INFORMATION FOR SEQ ID NO:39:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 631 amino acids	
	(B) TYPE: amino acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: protein	
	(v) FRAGMENT TYPE: internal	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
40	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
45	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
50	85 90 95	
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
55	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	

70

	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
	145					150					155					160
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
					165					170					175	
5	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
				180					185					190		
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
			195				200						205			
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
10		210					215					220				
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser
	225					230					235					240
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Thr	Met	Ala	Ala	Ala
					245					250					255	
15	Ala	Ala	Gln	Gly	Gly	Gly	Gly	Gly	Glu	Pro	Arg	Arg	Thr	Glu	Gly	Val
			260						265					270		
	Gly	Pro	Gly	Val	Pro	Gly	Glu	Val	Glu	Met	Val	Lys	Gly	Gln	Pro	Phe
			275					280					285			
	Asp	Val	Gly	Pro	Arg	Tyr	Thr	Gln	Leu	Gln	Tyr	Ile	Gly	Glu	Gly	Ala
20		290					295					300				
	Tyr	Gly	Met	Val	Ser	Ser	Ala	Tyr	Asp	His	Val	Arg	Lys	Thr	Arg	Val
	305					310					315					320
	Ala	Ile	Lys	Lys	Ile	Ser	Pro	Phe	Glu	His	Gln	Thr	Tyr	Cys	Gln	Arg
					325					330					335	
25	Thr	Leu	Arg	Glu	Ile	Gln	Ile	Leu	Leu	Arg	Phe	Arg	His	Glu	Asn	Val
			340						345					350		
	Ile	Gly	Ile	Arg	Asp	Ile	Leu	Arg	Ala	Ser	Thr	Leu	Glu	Ala	Met	Arg
			355					360					365			
	Asp	Val	Tyr	Ile	Val	Gln	Asp	Leu	Met	Glu	Thr	Asp	Leu	Tyr	Lys	Leu
30		370					375					380				
	Leu	Lys	Ser	Gln	Gln	Leu	Ser	Asn	Asp	His	Ile	Cys	Tyr	Phe	Leu	Tyr
	385					390					395					400
	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	Asn	Val	Leu	His
					405					410					415	
35	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Leu	Ser	Asn	Thr	Thr	Cys	Asp	Leu
				420					425					430		
	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Ile	Ala	Asp	Pro	Glu	His	Asp
			435					440					445			
	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg	Ala
40		450					455					460				
	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys	Gly	Tyr	Thr	Lys	Ser	Ile	Asp	Ile
	465					470					475					480
	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala	Glu	Met	Leu	Ser	Asn	Arg	Pro	Ile
					485					490					495	
45	Phe	Pro	Gly	Lys	His	Tyr	Leu	Asp	Gln	Leu	Asn	His	Ile	Leu	Gly	Ile
				500					505					510		
	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp	Leu	Asn	Cys	Ile	Ile	Asn	Met	Lys
			515					520					525			
	Ala	Arg	Asn	Tyr	Leu	Gln	Ser	Leu	Pro	Ser	Lys	Thr	Lys	Val	Ala	Trp
50		530					535					540				
	Ala	Lys	Leu	Phe	Pro	Lys	Ser	Asp	Ser	Lys	Ala	Leu	Asp	Leu	Leu	Asp
	545					550					555					560
	Arg	Met	Leu	Thr	Phe	Asn	Pro	Asn	Lys	Arg	Ile	Thr	Val	Glu	Glu	Ala
					565					570					575	
55	Leu	Ala	His	Pro	Tyr	Leu	Glu	Gln	Tyr	Tyr	Asp	Pro	Thr	Asp	Glu	Pro
				580					585					590		

70

71

Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp Leu Pro  
           595                                600                                605  
 Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg Phe Gln  
           610                                615                                620  
 5 Pro Gly Val Leu Glu Ala Pro  
     625                                630

## (2) INFORMATION FOR SEQ ID NO:40:

- 10 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 1818 base pairs  
     (B) TYPE: nucleic acid  
     (C) STRANDEDNESS: single  
     (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: cDNA  
     (ix) FEATURE:  
         (A) NAME/KEY: Coding Sequence  
         (B) LOCATION: 1...1815  
         (D) OTHER INFORMATION:
- 20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

25 ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
     1                                5                                10                                15

30 GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
                                 20                                25                                30

35 GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
                                 35                                40                                45

40 TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
                                 50                                55                                60

45 CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG 240  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
     65                                70                                75                                80

50 CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG 288  
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
                                 85                                90                                95

55 CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG 336  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
                                 100                                105                                110

GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC 384  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
     115                                120                                125

71

72

	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
5	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
10	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
15	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC	576
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
20	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG	624
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
	195 200 205	
25	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC	672
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
	210 215 220	
30	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC	720
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	
35	GGA CTC AGA TCT CGA GTA ACC ATG GCG GCG GCG GCG GCG GCG GGC CCG	768
	Gly Leu Arg Ser Arg Val Thr Met Ala Ala Ala Ala Ala Ala Gly Pro	
	245 250 255	
40	GAG ATG GTC CGC GGG CAG GTG TTC GAC GTG GGG CCG CGC TAC ACT AAT	816
	Glu Met Val Arg Gly Gln Val Phe Asp Val Gly Pro Arg Tyr Thr Asn	
	260 265 270	
45	CTC TCG TAC ATC GGA GAA GGC GCC TAC GGC ATG GTT TGT TCT GCT TAT	864
	Leu Ser Tyr Ile Gly Glu Gly Ala Tyr Gly Met Val Cys Ser Ala Tyr	
	275 280 285	
50	GAT AAT CTC AAC AAA GTT CGA GTT GCT ATC AAG AAA ATC AGT CCT TTT	912
	Asp Asn Leu Asn Lys Val Arg Val Ala Ile Lys Lys Ile Ser Pro Phe	
	290 295 300	
55	GAG CAC CAG ACC TAC TGT CAG AGA ACC CTG AGA GAG ATA AAA ATC CTA	960
	Glu His Gln Thr Tyr Cys Gln Arg Thr Leu Arg Glu Ile Lys Ile Leu	
	305 310 315 320	
50	CTG CGC TTC AGA CAT GAG AAC ATC ATC GGC ATC AAT GAC ATC ATC CGG	1008
	Leu Arg Phe Arg His Glu Asn Ile Ile Gly Ile Asn Asp Ile Ile Arg	
	325 330 335	
55	GCA CCA ACC ATT GAG CAG ATG AAA GAT GTA TAT ATA GTA CAG GAC CTC	1056
	Ala Pro Thr Ile Glu Gln Met Lys Asp Val Tyr Ile Val Gln Asp Leu	
	340 345 350	

73

	ATG GAG ACA GAT CTT TAC AAG CTC TTG AAG ACA CAG CAC CTC AGC AAT	1104
	Met Glu Thr Asp Leu Tyr Lys Leu Leu Lys Thr Gln His Leu Ser Asn	
	355 360 365	
5	GAT CAT ATC TGC TAT TTT CTT TAT CAG ATC CTG AGA GGA TTA AAG TAT	1152
	Asp His Ile Cys Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr	
	370 375 380	
10	ATA CAT TCA GCT AAT GTT CTG CAC CGT GAC CTC AAG CCT TCC AAC CTC	1200
	Ile His Ser Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu	
	385 390 395 400	
15	CTG CTG AAC ACC ACT TGT GAT CTC AAG ATC TGT GAC TTT GGC CTT GCC	1248
	Leu Leu Asn Thr Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala	
	405 410 415	
20	CGT GTT GCA GAT CCA GAC CAT GAT CAT ACA GGG TTC TTG ACA GAG TAT	1296
	Arg Val Ala Asp Pro Asp His Asp His Thr Gly Phe Leu Thr Glu Tyr	
	420 425 430	
	GTA GCC ACG CGT TGG TAC AGA GCT CCA GAA ATT ATG TTG AAT TCC AAG	1344
	Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys	
	435 440 445	
25	GGT TAT ACC AAG TCC ATT GAT ATT TGG TCT GTG GGC TGC ATC CTG GCA	1392
	Gly Tyr Thr Lys Ser Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala	
	450 455 460	
30	GAG ATG CTA TCC AAC AGG CCT ATC TTC CCA GGA AAG CAT TAC CTT GAC	1440
	Glu Met Leu Ser Asn Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp	
	465 470 475 480	
35	CAG CTG AAT CAC ATC CTG GGT ATT CTT GGA TCT CCA TCA CAG GAA GAT	1488
	Gln Leu Asn His Ile Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp	
	485 490 495	
40	CTG AAT TGT ATA ATA AAT TTA AAA GCT AGA AAC TAT TTG CTT TCT CTC	1536
	Leu Asn Cys Ile Ile Asn Leu Lys Ala Arg Asn Tyr Leu Leu Ser Leu	
	500 505 510	
	CCG CAC AAA AAT AAG GTG CCG TGG AAC AGG TTG TTC CCA AAC GCT GAC	1584
	Pro His Lys Asn Lys Val Pro Trp Asn Arg Leu Phe Pro Asn Ala Asp	
	515 520 525	
45	TCC AAA GCT CTG GAT TTA CTG GAT AAA ATG TTG ACA TTT AAC CCT CAC	1632
	Ser Lys Ala Leu Asp Leu Leu Asp Lys Met Leu Thr Phe Asn Pro His	
	530 535 540	
50	AAG AGG ATT GAA GTT GAA CAG GCT CTG GCC CAC CCG TAC CTG GAG CAG	1680
	Lys Arg Ile Glu Val Glu Gln Ala Leu Ala His Pro Tyr Leu Glu Gln	
	545 550 555 560	
55	TAT TAT GAC CCA AGT GAT GAG CCC ATT GCT GAA GCA CCA TTC AAG TTT	1728
	Tyr Tyr Asp Pro Ser Asp Glu Pro Ile Ala Glu Ala Pro Phe Lys Phe	
	565 570 575	

74

GAC ATG GAG CTG GAC GAC TTA CCT AAG GAG AAG CTC AAA GAA CTC ATT 1776  
 Asp Met Glu Leu Asp Asp Leu Pro Lys Glu Lys Leu Lys Glu Leu Ile  
 580 585 590

5 TTT GAA GAG ACT GCT CGA TTC CAG CCA GGA TAC AGA TCT TAA 1818  
 Phe Glu Glu Thr Ala Arg Phe Gln Pro Gly Tyr Arg Ser  
 595 600 605

10 (2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 605 amino acids

(B) TYPE: amino acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 25 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 30 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 35 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 40 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175  
 45 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190  
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
 195 200 205  
 50 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220  
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser  
 225 230 235 240  
 Gly Leu Arg Ser Arg Val Thr Met Ala Ala Ala Ala Ala Gly Pro  
 245 250 255  
 55 Glu Met Val Arg Gly Gln Val Phe Asp Val Gly Pro Arg Tyr Thr Asn  
 260 265 270

74

75

Leu Ser Tyr Ile Gly Glu Gly Ala Tyr Gly Met Val Cys Ser Ala Tyr  
 275 280 285  
 Asp Asn Leu Asn Lys Val Arg Val Ala Ile Lys Lys Ile Ser Pro Phe  
 290 295 300  
 5 Glu His Gln Thr Tyr Cys Gln Arg Thr Leu Arg Glu Ile Lys Ile Leu  
 305 310 315 320  
 Leu Arg Phe Arg His Glu Asn Ile Ile Gly Ile Asn Asp Ile Ile Arg  
 325 330 335  
 10 Ala Pro Thr Ile Glu Gln Met Lys Asp Val Tyr Ile Val Gln Asp Leu  
 340 345 350  
 Met Glu Thr Asp Leu Tyr Lys Leu Leu Lys Thr Gln His Leu Ser Asn  
 355 360 365  
 Asp His Ile Cys Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr  
 370 375 380  
 15 Ile His Ser Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu  
 385 390 395 400  
 Leu Leu Asn Thr Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala  
 405 410 415  
 20 Arg Val Ala Asp Pro Asp His Asp His Thr Gly Phe Leu Thr Glu Tyr  
 420 425 430  
 Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys  
 435 440 445  
 Gly Tyr Thr Lys Ser Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala  
 450 455 460  
 25 Glu Met Leu Ser Asn Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp  
 465 470 475 480  
 Gln Leu Asn His Ile Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp  
 485 490 495  
 30 Leu Asn Cys Ile Ile Asn Leu Lys Ala Arg Asn Tyr Leu Leu Ser Leu  
 500 505 510  
 Pro His Lys Asn Lys Val Pro Trp Asn Arg Leu Phe Pro Asn Ala Asp  
 515 520 525  
 Ser Lys Ala Leu Asp Leu Leu Asp Lys Met Leu Thr Phe Asn Pro His  
 530 535 540  
 35 Lys Arg Ile Glu Val Glu Gln Ala Leu Ala His Pro Tyr Leu Glu Gln  
 545 550 555 560  
 Tyr Tyr Asp Pro Ser Asp Glu Pro Ile Ala Glu Ala Pro Phe Lys Phe  
 565 570 575  
 40 Asp Met Glu Leu Asp Asp Leu Pro Lys Glu Lys Leu Lys Glu Leu Ile  
 580 585 590  
 Phe Glu Glu Thr Ala Arg Phe Gln Pro Gly Tyr Arg Ser  
 595 600 605

(2) INFORMATION FOR SEQ ID NO:42:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2529 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

50

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

55

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2526

75

76

## (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

5	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
10	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
15	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
20	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
25	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
30	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
35	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
40	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
45	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
50	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
55	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
55	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC	576
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
55	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG	624
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
	195 200 205	

76



77

	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC	672
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
	210 215 220	
5	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC	720
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	
10	GGA CTC AGA TCT CGA GCT CAA GCT TCG AAT TCG TCA ATG GAG CTG GAA	768
	Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ser Met Glu Leu Glu	
	245 250 255	
15	AAC ATC GTG GCC AAC ACG GTC TTG CTG AAA GCC AGG GAA GGG GGC GGA	816
	Asn Ile Val Ala Asn Thr Val Leu Leu Lys Ala Arg Glu Gly Gly Gly	
	260 265 270	
20	GGA AAG CGC AAA GGG AAA AGC AAG AAG TGG AAA GAA ATC CTG AAG TTC	864
	Gly Lys Arg Lys Gly Lys Ser Lys Lys Trp Lys Glu Ile Leu Lys Phe	
	275 280 285	
25	CCT CAC ATT AGC CAG TGT GAA GAC CTC CGA AGG ACC ATA GAC AGA GAT	912
	Pro His Ile Ser Gln Cys Glu Asp Leu Arg Arg Thr Ile Asp Arg Asp	
	290 295 300	
30	TAC TGC AGT TTA TGT GAC AAG CAG CCA ATC GGG AGG CTG CTT TTC CGG	960
	Tyr Cys Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg Leu Leu Phe Arg	
	305 310 315 320	
35	CAG TTT TGT GAA ACC AGG CCT GGG CTG GAG TGT TAC ATT CAG TTC CTG	1008
	Gln Phe Cys Glu Thr Arg Pro Gly Leu Glu Cys Tyr Ile Gln Phe Leu	
	325 330 335	
40	GAC TCC GTG GCA GAA TAT GAA GTT ACT CCA GAT GAA AAA CTG GGA GAG	1056
	Asp Ser Val Ala Glu Tyr Glu Val Thr Pro Asp Glu Lys Leu Gly Glu	
	340 345 350	
45	AAA GGG AAG GAA ATT ATG ACC AAG TAC CTC ACC CCA AAG TCC CCT GTT	1104
	Lys Gly Lys Glu Ile Met Thr Lys Tyr Leu Thr Pro Lys Ser Pro Val	
	355 360 365	
50	TTC ATA GCC CAA GTT GGC CAA GAC CTG GTC TCC CAG ACG GAG GAG AAG	1152
	Phe Ile Ala Gln Val Gly Gln Asp Leu Val Ser Gln Thr Glu Glu Lys	
	370 375 380	
55	CTC CTA CAG AAG CCG TGC AAA GAA CTC TTT TCT GCC TGT GCA CAG TCT	1200
	Leu Leu Gln Lys Pro Cys Lys Glu Leu Phe Ser Ala Cys Ala Gln Ser	
	385 390 395 400	
55	GTC CAC GAG TAC CTG AGG GGA GAA CCA TTC CAC GAA TAT CTG GAC AGC	1248
	Val His Glu Tyr Leu Arg Gly Glu Pro Phe His Glu Tyr Leu Asp Ser	
	405 410 415	
55	ATG TTT TTT GAC CGC TTT CTC CAG TGG AAG TGG TTG GAA AGG CAA CCG	1296
	Met Phe Phe Asp Arg Phe Leu Gln Trp Lys Trp Leu Glu Arg Gln Pro	
	420 425 430	

78

	GTG ACC AAA AAC ACT TTC AGG CAG TAT CGA GTG CTA GGA AAA GGG GGC	1344
	Val Thr Lys Asn Thr Phe Arg Gln Tyr Arg Val Leu Gly Lys Gly Gly	
	435 440 445	
5	TTC GGG GAG GTC TGT GCC TGC CAG GTT CGG GCC ACG GGT AAA ATG TAT	1392
	Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala Thr Gly Lys Met Tyr	
	450 455 460	
10	GCC TGC AAG CGC TTG GAG AAG AAG AGG ATC AAA AAG AGG AAA GGG GAG	1440
	Ala Cys Lys Arg Leu Glu Lys Lys Arg Ile Lys Lys Arg Lys Gly Glu	
	465 470 475 480	
15	TCC ATG GCC CTC AAT GAG AAG CAG ATC CTC GAG AAG GTC AAC AGT CAG	1488
	Ser Met Ala Leu Asn Glu Lys Gln Ile Leu Glu Lys Val Asn Ser Gln	
	485 490 495	
20	TTT GTG GTC AAC CTG GCC TAT GCC TAC GAG ACC AAG GAT GCA CTG TGC	1536
	Phe Val Val Asn Leu Ala Tyr Ala Tyr Glu Thr Lys Asp Ala Leu Cys	
	500 505 510	
25	TTG GTC CTG ACC ATC ATG AAT GGG GGT GAC CTG AAG TTC CAC ATC TAC	1584
	Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu Lys Phe His Ile Tyr	
	515 520 525	
30	AAC ATG GGC AAC CCT GGC TTC GAG GAG GAG CGG GCC TTG TTT TAT GCG	1632
	Asn Met Gly Asn Pro Gly Phe Glu Glu Glu Arg Ala Leu Phe Tyr Ala	
	530 535 540	
35	GCA GAG ATC CTC TGC GGC TTA GAA GAC CTC CAC CGT GAG AAC ACC GTC	1680
	Ala Glu Ile Leu Cys Gly Leu Glu Asp Leu His Arg Glu Asn Thr Val	
	545 550 555 560	
40	TAC CGA GAT CTG AAA CCT GAA AAC ATC CTG TTA GAT GAT TAT GGC CAC	1728
	Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Asp Tyr Gly His	
	565 570 575	
45	ATT AGG ATC TCA GAC CTG GGC TTG GCT GTG AAG ATC CCC GAG GGA GAC	1776
	Ile Arg Ile Ser Asp Leu Gly Leu Ala Val Lys Ile Pro Glu Gly Asp	
	580 585 590	
50	CTG ATC CGC GGC CGG GTG GGC ACT GTT GGC TAC ATG GCC CCC GAA GTC	1824
	Leu Ile Arg Gly Arg Val Gly Thr Val Gly Tyr Met Ala Pro Glu Val	
	595 600 605	
55	CTG AAC AAC CAG AGG TAC GGC CTG AGC CCC GAC TAC TGG GGC CTT GGC	1872
	Leu Asn Asn Gln Arg Tyr Gly Leu Ser Pro Asp Tyr Trp Gly Leu Gly	
	610 615 620	
60	TGC CTC ATC TAT GAG ATG ATC GAG GGC CAG TCG CCG TTC CGC GGC CGT	1920
	Cys Leu Ile Tyr Glu Met Ile Glu Gly Gln Ser Pro Phe Arg Gly Arg	
	625 630 635 640	
65	AAG GAG AAG GTG AAG CGG GAG GAG GTG GAC CGC CGG GTC CTG GAG ACG	1968
	Lys Glu Lys Val Lys Arg Glu Glu Val Asp Arg Arg Val Leu Glu Thr	
	645 650 655	

79

	GAG GAG GTG TAC TCC CAC AAG TTC TCC GAG GAG GCC AAG TCC ATC TGC	2016
	Glu Glu Val Tyr Ser His Lys Phe Ser Glu Glu Ala Lys Ser Ile Cys	
	660 665 670	
5	AAG ATG CTG CTC ACG AAA GAT GCG AAG CAG AGG CTG GGC TGC CAG GAG	2064
	Lys Met Leu Leu Thr Lys Asp Ala Lys Gln Arg Leu Gly Cys Gln Glu	
	675 680 685	
10	GAG GGG GCT GCA GAG GTC AAG AGA CAC CCC TTC TTC AGG AAC ATG AAC	2112
	Glu Gly Ala Ala Glu Val Lys Arg His Pro Phe Phe Arg Asn Met Asn	
	690 695 700	
15	TTC AAG CGC TTA GAA GCC GGG ATG TTG GAC CCT CCC TTC GTT CCA GAC	2160
	Phe Lys Arg Leu Glu Ala Gly Met Leu Asp Pro Pro Phe Val Pro Asp	
	705 710 715 720	
20	CCC CGC GCT GTG TAC TGT AAG GAC GTG CTG GAC ATC GAG CAG TTC TCC	2208
	Pro Arg Ala Val Tyr Cys Lys Asp Val Leu Asp Ile Glu Gln Phe Ser	
	725 730 735	
25	ACT GTG AAG GGC GTC AAT CTG GAC CAC ACA GAC GAC GAC TTC TAC TCC	2256
	Thr Val Lys Gly Val Asn Leu Asp His Thr Asp Asp Asp Phe Tyr Ser	
	740 745 750	
30	AAG TTC TCC ACG GGC TCT GTG TCC ATC CCA TGG CAA AAC GAG ATG ATA	2304
	Lys Phe Ser Thr Gly Ser Val Ser Ile Pro Trp Gln Asn Glu Met Ile	
	755 760 765	
35	GAA ACA GAA TGC TTT AAG GAG CTG AAC GTG TTT GGA CCT AAT GGT ACC	2352
	Glu Thr Glu Cys Phe Lys Glu Leu Asn Val Phe Gly Pro Asn Gly Thr	
	770 775 780	
40	CTC CCG CCA GAT CTG AAC AGA AAC CAC CCT CCG GAA CCG CCC AAG AAA	2400
	Leu Pro Pro Asp Leu Asn Arg Asn His Pro Pro Glu Pro Pro Lys Lys	
	785 790 795 800	
45	GGG CTG CTC CAG AGA CTC TTC AAG CGG CAG CAT CAG AAC AAT TCC AAG	2448
	Gly Leu Leu Gln Arg Leu Phe Lys Arg Gln His Gln Asn Asn Ser Lys	
	805 810 815	
50	AGT TCG CCC AGC TCC AAG ACC AGT TTT AAC CAC CAC ATA AAC TCA AAC	2496
	Ser Ser Pro Ser Ser Lys Thr Ser Phe Asn His His Ile Asn Ser Asn	
	820 825 830	
55	CAT GTC AGC TCG AAC TCC ACC GGA AGC AGC TAG	2529
	His Val Ser Ser Asn Ser Thr Gly Ser Ser	
	835 840	

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 842 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1           5           10           15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
10           20           25           30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35           40           45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50           55           60
15 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65           70           75           80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85           90           95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
20           100          105          110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115          120          125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130          135          140
25 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145          150          155          160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165          170          175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
30           180          185          190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195          200          205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210          215          220
35 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225          230          235          240
Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ser Met Glu Leu Glu
 245          250          255
Asn Ile Val Ala Asn Thr Val Leu Leu Lys Ala Arg Glu Gly Gly Gly
40           260          265          270
Gly Lys Arg Lys Gly Lys Ser Lys Lys Trp Lys Glu Ile Leu Lys Phe
 275          280          285
Pro His Ile Ser Gln Cys Glu Asp Leu Arg Arg Thr Ile Asp Arg Asp
 290          295          300
45 Tyr Cys Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg Leu Leu Phe Arg
 305          310          315          320
Gln Phe Cys Glu Thr Arg Pro Gly Leu Glu Cys Tyr Ile Gln Phe Leu
 325          330          335
Asp Ser Val Ala Glu Tyr Glu Val Thr Pro Asp Glu Lys Leu Gly Glu
50           340          345          350
Lys Gly Lys Glu Ile Met Thr Lys Tyr Leu Thr Pro Lys Ser Pro Val
 355          360          365
Phe Ile Ala Gln Val Gly Gln Asp Leu Val Ser Gln Thr Glu Glu Lys
 370          375          380
55 Leu Leu Gln Lys Pro Cys Lys Glu Leu Phe Ser Ala Cys Ala Gln Ser
 385          390          395          400

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81

	Val	His	Glu	Tyr	Leu	Arg	Gly	Glu	Pro	Phe	His	Glu	Tyr	Leu	Asp	Ser
					405					410					415	
	Met	Phe	Phe	Asp	Arg	Phe	Leu	Gln	Trp	Lys	Trp	Leu	Glu	Arg	Gln	Pro
				420					425					430		
5	Val	Thr	Lys	Asn	Thr	Phe	Arg	Gln	Tyr	Arg	Val	Leu	Gly	Lys	Gly	Gly
			435					440					445			
	Phe	Gly	Glu	Val	Cys	Ala	Cys	Gln	Val	Arg	Ala	Thr	Gly	Lys	Met	Tyr
		450					455					460				
10	Ala	Cys	Lys	Arg	Leu	Glu	Lys	Lys	Arg	Ile	Lys	Lys	Arg	Lys	Gly	Glu
	465				470					475						480
	Ser	Met	Ala	Leu	Asn	Glu	Lys	Gln	Ile	Leu	Glu	Lys	Val	Asn	Ser	Gln
				485					490					495		
	Phe	Val	Val	Asn	Leu	Ala	Tyr	Ala	Tyr	Glu	Thr	Lys	Asp	Ala	Leu	Cys
				500					505					510		
15	Leu	Val	Leu	Thr	Ile	Met	Asn	Gly	Gly	Asp	Leu	Lys	Phe	His	Ile	Tyr
		515						520					525			
	Asn	Met	Gly	Asn	Pro	Gly	Phe	Glu	Glu	Glu	Arg	Ala	Leu	Phe	Tyr	Ala
		530					535					540				
20	Ala	Glu	Ile	Leu	Cys	Gly	Leu	Glu	Asp	Leu	His	Arg	Glu	Asn	Thr	Val
	545				550					555						560
	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Ile	Leu	Leu	Asp	Asp	Tyr	Gly	His
				565					570						575	
	Ile	Arg	Ile	Ser	Asp	Leu	Gly	Leu	Ala	Val	Lys	Ile	Pro	Glu	Gly	Asp
				580					585					590		
25	Leu	Ile	Arg	Gly	Arg	Val	Gly	Thr	Val	Gly	Tyr	Met	Ala	Pro	Glu	Val
		595					600						605			
	Leu	Asn	Asn	Gln	Arg	Tyr	Gly	Leu	Ser	Pro	Asp	Tyr	Trp	Gly	Leu	Gly
		610					615					620				
30	Cys	Leu	Ile	Tyr	Glu	Met	Ile	Glu	Gly	Gln	Ser	Pro	Phe	Arg	Gly	Arg
	625				630					635						640
	Lys	Glu	Lys	Val	Lys	Arg	Glu	Glu	Val	Asp	Arg	Arg	Val	Leu	Glu	Thr
				645					650					655		
	Glu	Glu	Val	Tyr	Ser	His	Lys	Phe	Ser	Glu	Glu	Ala	Lys	Ser	Ile	Cys
				660					665					670		
35	Lys	Met	Leu	Leu	Thr	Lys	Asp	Ala	Lys	Gln	Arg	Leu	Gly	Cys	Gln	Glu
		675						680					685			
	Glu	Gly	Ala	Ala	Glu	Val	Lys	Arg	His	Pro	Phe	Phe	Arg	Asn	Met	Asn
		690					695					700				
40	Phe	Lys	Arg	Leu	Glu	Ala	Gly	Met	Leu	Asp	Pro	Pro	Phe	Val	Pro	Asp
	705				710					715						720
	Pro	Arg	Ala	Val	Tyr	Cys	Lys	Asp	Val	Leu	Asp	Ile	Glu	Gln	Phe	Ser
				725					730						735	
	Thr	Val	Lys	Gly	Val	Asn	Leu	Asp	His	Thr	Asp	Asp	Asp	Phe	Tyr	Ser
				740					745					750		
45	Lys	Phe	Ser	Thr	Gly	Ser	Val	Ser	Ile	Pro	Trp	Gln	Asn	Glu	Met	Ile
		755						760					765			
	Glu	Thr	Glu	Cys	Phe	Lys	Glu	Leu	Asn	Val	Phe	Gly	Pro	Asn	Gly	Thr
		770					775					780				
50	Leu	Pro	Pro	Asp	Leu	Asn	Arg	Asn	His	Pro	Pro	Glu	Pro	Pro	Lys	Lys
	785				790					795						800
	Gly	Leu	Leu	Gln	Arg	Leu	Phe	Lys	Arg	Gln	His	Gln	Asn	Asn	Ser	Lys
				805					810						815	
	Ser	Ser	Pro	Ser	Ser	Lys	Thr	Ser	Phe	Asn	His	His	Ile	Asn	Ser	Asn
				820					825					830		
55	His	Val	Ser	Ser	Asn	Ser	Thr	Gly	Ser	Ser						
			835					840								

81

## (2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 1902 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...1899  
15 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

20	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
25	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
30	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
35	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
40	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
45	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
50	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
60	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
65	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	

83

	145	150	155	160	
5	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	165	170	175	528
10	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	180	185	190	576
15	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	195	200	205	624
20	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	210	215	220	672
25	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	225	230	235	720
30	GGA CTC AGA TCT CGA GCT CGA GCC ATC ATG AGC AGA AGC AAG CGT GAC Gly Leu Arg Ser Arg Ala Arg Ala Ile Met Ser Arg Ser Lys Arg Asp	245	250	255	768
35	AAC AAT TTT TAT AGT GTA GAG ATT GGA GAT TCT ACA TTC ACA GTC CTG Asn Asn Phe Tyr Ser Val Glu Ile Gly Asp Ser Thr Phe Thr Val Leu	260	265	270	816
40	AAA CGA TAT CAG AAT TTA AAA CCT ATA GGC TCA GGA GCT CAA GGA ATA Lys Arg Tyr Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile	275	280	285	864
45	GTA TGC GCA GCT TAT GAT GCC ATT CTT GAA AGA AAT GTT GCA ATC AAG Val Cys Ala Ala Tyr Asp Ala Ile Leu Glu Arg Asn Val Ala Ile Lys	290	295	300	912
50	AAG CTA AGC CGA CCA TTT CAG AAT CAG ACT CAT GCC AAG CGG GCC TAC Lys Leu Ser Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr	305	310	315	960
55	AGA GAG CTA GTT CTT ATG AAA TGT GTT AAT CAC AAA AAT ATA ATT GGC Arg Glu Leu Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Gly	325	330	335	1008
60	CTT TTG AAT GTT TTC ACA CCA CAG AAA TCC CTA GAA GAA TTT CAA GAT Leu Leu Asn Val Phe Thr Pro Gln Lys Ser Leu Glu Glu Phe Gln Asp	340	345	350	1056
65	GTT TAC ATA GTC ATG GAG CTC ATG GAT GCA AAT CTT TGC CAA GTG ATT Val Tyr Ile Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile	355	360	365	1104
70	CAG ATG GAG CTA GAT CAT GAA AGA ATG TCC TAC CTT CTC TAT CAG ATG Gln Met Glu Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met				1152

84

	370	375	380	
5	CTG TGT GGA ATC AAG CAC CTT CAT TCT GCT GGA ATT ATT CAT CGG GAC Leu Cys Gly Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp 385 390 395 400	1200		
10	TTA AAG CCC AGT AAT ATA GTA GTA AAA TCT GAT TGC ACT TTG AAG ATT Leu Lys Pro Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile 405 410 415	1248		
15	CTT GAC TTC GGT CTG GCC AGG ACT GCA GGA ACG AGT TTT ATG ATG ACG Leu Asp Phe Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr 420 425 430	1296		
20	CCT TAT GTA GTG ACT CGC TAC TAC AGA GCA CCC GAG GTC ATC CTT GGC Pro Tyr Val Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly 435 440 445	1344		
25	ATG GGC TAC AAG GAA AAC GTG GAT TTA TGG TCT GTG GGG TGC ATT ATG Met Gly Tyr Lys Glu Asn Val Asp Leu Trp Ser Val Gly Cys Ile Met 450 455 460	1392		
30	GGA GAA ATG GTT TGC CAC AAA ATC CTC TTT CCA GGA AGG GAC TAT ATT Gly Glu Met Val Cys His Lys Ile Leu Phe Pro Gly Arg Asp Tyr Ile 465 470 475 480	1440		
35	GAT CAG TGG AAT AAA GTT ATT GAA CAG CTT GGA ACA CCA TGT CCT GAA Asp Gln Trp Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu 485 490 495	1488		
40	TTC ATG AAG AAA CTG CAA CCA ACA GTA AGG ACT TAC GTT GAA AAC AGA Phe Met Lys Lys Leu Gln Pro Thr Val Arg Thr Tyr Val Glu Asn Arg 500 505 510	1536		
45	CCT AAA TAT GCT GGA TAT AGC TTT GAG AAA CTC TTC CCT GAT GTC CTT Pro Lys Tyr Ala Gly Tyr Ser Phe Glu Lys Leu Phe Pro Asp Val Leu 515 520 525	1584		
50	TTC CCA GCT GAC TCA GAA CAC AAC AAA CTT AAA GCC AGT CAG GCA AGG Phe Pro Ala Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg 530 535 540	1632		
55	GAT TTG TTA TCC AAA ATG CTG GTA ATA GAT GCA TCT AAA AGG ATC TCT Asp Leu Leu Ser Lys Met Leu Val Ile Asp Ala Ser Lys Arg Ile Ser 545 550 555 560	1680		
60	GTA GAT GAA GCT CTC CAA CAC CCG TAC ATC AAT GTC TGG TAT GAT CCT Val Asp Glu Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro 565 570 575	1728		
65	TCT GAA GCA GAA GCT CCA CCA CCA AAG ATC CCT GAC AAG CAG TTA GAT Ser Glu Ala Glu Ala Pro Pro Pro Lys Ile Pro Asp Lys Gln Leu Asp 580 585 590	1776		
70	GAA AGG GAA CAC ACA ATA GAA GAG TGG AAA GAA TTG ATA TAT AAG GAA Glu Arg Glu His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu	1824		



85

595 600 605

GTT ATG GAC TTG GAG GAG AGA ACC AAG AAT GGA GTT ATA CGG GGG CAG 1872  
 Val Met Asp Leu Glu Glu Arg Thr Lys Asn Gly Val Ile Arg Gly Gln  
 5 610 615 620

CCC TCT CCT TTA GCA CAG GTG CAG CAG TGA 1902  
 Pro Ser Pro Leu Ala Gln Val Gln Gln  
 10 625 630

## (2) INFORMATION FOR SEQ ID NO:45:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 633 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

25 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 30 35 40 45  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 35 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 40 115 120 125  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
 45 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190  
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
 50 195 200 205  
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220  
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser  
 225 230 235 240  
 55 Gly Leu Arg Ser Arg Ala Arg Ala Ile Met Ser Arg Ser Lys Arg Asp  
 245 250 255

85

86

Asn Asn Phe Tyr Ser Val Glu Ile Gly Asp Ser Thr Phe Thr Val Leu  
 260 265 270  
 Lys Arg Tyr Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile  
 275 280 285  
 5 Val Cys Ala Ala Tyr Asp Ala Ile Leu Glu Arg Asn Val Ala Ile Lys  
 290 295 300  
 Lys Leu Ser Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr  
 305 310 315 320  
 10 Arg Glu Leu Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Gly  
 325 330 335  
 Leu Leu Asn Val Phe Thr Pro Gln Lys Ser Leu Glu Glu Phe Gln Asp  
 340 345 350  
 Val Tyr Ile Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile  
 355 360 365  
 15 Gln Met Glu Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met  
 370 375 380  
 Leu Cys Gly Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp  
 385 390 395 400  
 20 Leu Lys Pro Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile  
 405 410 415  
 Leu Asp Phe Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr  
 420 425 430  
 Pro Tyr Val Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly  
 435 440 445  
 25 Met Gly Tyr Lys Glu Asn Val Asp Leu Trp Ser Val Gly Cys Ile Met  
 450 455 460  
 Gly Glu Met Val Cys His Lys Ile Leu Phe Pro Gly Arg Asp Tyr Ile  
 465 470 475 480  
 30 Asp Gln Trp Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu  
 485 490 495  
 Phe Met Lys Lys Leu Gln Pro Thr Val Arg Thr Tyr Val Glu Asn Arg  
 500 505 510  
 Pro Lys Tyr Ala Gly Tyr Ser Phe Glu Lys Leu Phe Pro Asp Val Leu  
 515 520 525  
 35 Phe Pro Ala Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg  
 530 535 540  
 Asp Leu Leu Ser Lys Met Leu Val Ile Asp Ala Ser Lys Arg Ile Ser  
 545 550 555 560  
 Val Asp Glu Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro  
 565 570 575  
 40 Ser Glu Ala Glu Ala Pro Pro Pro Lys Ile Pro Asp Lys Gln Leu Asp  
 580 585 590  
 Glu Arg Glu His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu  
 595 600 605  
 45 Val Met Asp Leu Glu Glu Arg Thr Lys Asn Gly Val Ile Arg Gly Gln  
 610 615 620  
 Pro Ser Pro Leu Ala Gln Val Gln Gln  
 625 630

50 (2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1824 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

86

87

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 5 (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...1821  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

10  
 ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

15  
 GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

20  
 GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

25  
 TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

30  
 CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG 240  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

35  
 CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG 288  
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

40  
 CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG 336  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

45  
 GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC 384  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125

50  
 ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC 432  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140

55  
 AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC 480  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160

60  
 GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC 528  
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175

65  
 GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC 576  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly

87

88

	180	185	190	
5	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205	624		
10	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220	672		
15	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225 230 235 240	720		
20	GGA CTC AGA TCT CGA GGG AAA ATG TCT CAG GAG AGG CCC ACG TTC TAC Gly Leu Arg Ser Arg Gly Lys Met Ser Gln Glu Arg Pro Thr Phe Tyr 245 250 255	768		
25	CGG CAG GAG CTG AAC AAG ACA ATC TGG GAG GTG CCC GAG CGT TAC CAG Arg Gln Glu Leu Asn Lys Thr Ile Trp Glu Val Pro Glu Arg Tyr Gln 260 265 270	816		
30	AAC CTG TCT CCA GTG GGC TCT GGC GCC TAT GGC TCT GTG TGT GCT GCT Asn Leu Ser Pro Val Gly Ser Gly Ala Tyr Gly Ser Val Cys Ala Ala 275 280 285	864		
35	TTT GAC ACA AAA ACG GGG TTA CGT GTG GCA GTG AAG AAG CTC TCC AGA Phe Asp Thr Lys Thr Gly Leu Arg Val Ala Val Lys Lys Leu Ser Arg 290 295 300	912		
40	CCA TTT CAG TCC ATC ATT CAT GCG AAA AGA ACC TAC AGA GAA CTG CGG Pro Phe Gln Ser Ile Ile His Ala Lys Arg Thr Tyr Arg Glu Leu Arg 305 310 315 320	960		
45	TTA CTT AAA CAT ATG AAA CAT GAA AAT GTG ATT GGT CTG TTG GAC GTT Leu Leu Lys His Met Lys His Glu Asn Val Ile Gly Leu Leu Asp Val 325 330 335	1008		
50	TTT ACA CCT GCA AGG TCT CTG GAG GAA TTC AAT GAT GTG TAT CTG GTG Phe Thr Pro Ala Arg Ser Leu Glu Glu Phe Asn Asp Val Tyr Leu Val 340 345 350	1056		
55	ACC CAT CTC ATG GGG GCA GAT CTG AAC AAC ATT GTG AAA TGT CAG AAG Thr His Leu Met Gly Ala Asp Leu Asn Asn Ile Val Lys Cys Gln Lys 355 360 365	1104		
60	CTT ACA GAT GAC CAT GTT CAG TTC CTT ATC TAC CAA ATT CTC CGA GGT Leu Thr Asp Asp His Val Gln Phe Leu Ile Tyr Gln Ile Leu Arg Gly 370 375 380	1152		
65	CTA AAG TAT ATA CAT TCA GCT GAC ATA ATT CAC AGG GAC CTA AAA CCT Leu Lys Tyr Ile His Ser Ala Asp Ile Ile His Arg Asp Leu Lys Pro 385 390 395 400	1200		
70	AGT AAT CTA GCT GTG AAT GAA GAC TGT GAG CTG AAG ATT CTG GAT TTT Ser Asn Leu Ala Val Asn Glu Asp Cys Glu Leu Lys Ile Leu Asp Phe 1248			

		405	89	410	415	
5		GGA CTG GCT CGG CAC ACA GAT GAT GAA ATG ACA GGC TAC GTG GCC ACT Gly Leu Ala Arg His Thr Asp Asp Glu Met Thr Gly Tyr Val Ala Thr	1296			
		420	425	430		
10		AGG TGG TAC AGG GCT CCT GAG ATC ATG CTG AAC TGG ATG CAT TAC AAC Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Trp Met His Tyr Asn	1344			
		435	440	445		
15		CAG ACA GTT GAT ATT TGG TCA GTG GGA TGC ATA ATG GCC GAG CTG TTG Gln Thr Val Asp Ile Trp Ser Val Gly Cys Ile Met Ala Glu Leu Leu	1392			
		450	455	460		
20		ACT GGA AGA ACA TTG TTT CCT GGT ACA GAC CAT ATT GAT CAG TTG AAG Thr Gly Arg Thr Leu Phe Pro Gly Thr Asp His Ile Asp Gln Leu Lys	1440			
		465	470	475	480	
25		CTC ATT TTA AGA CTC GTT GGA ACC CCA GGG GCT GAG CTT TTG AAG AAA Leu Ile Leu Arg Leu Val Gly Thr Pro Gly Ala Glu Leu Leu Lys Lys	1488			
		485	490	495		
30		ATC TCC TCA GAG TCT GCA AGA AAC TAT ATT CAG TCT TTG ACT CAG ATG Ile Ser Ser Glu Ser Ala Arg Asn Tyr Ile Gln Ser Leu Thr Gln Met	1536			
		500	505	510		
35		CCG AAG ATG AAC TTT GCG AAT GTA TTT ATT GGT GCC AAT CCC CTG GCT Pro Lys Met Asn Phe Ala Asn Val Phe Ile Gly Ala Asn Pro Leu Ala	1584			
		515	520	525		
40		GTC GAC TTG CTG GAG AAG ATG CTT GTA TTG GAC TCA GAT AAG AGA ATT Val Asp Leu Leu Glu Lys Met Leu Val Leu Asp Ser Asp Lys Arg Ile	1632			
		530	535	540		
45		ACA GCG GCC CAA GCC CTT GCA CAT GCC TAC TTT GCT CAG TAC CAC GAT Thr Ala Ala Gln Ala Leu Ala His Ala Tyr Phe Ala Gln Tyr His Asp	1680			
		545	550	555	560	
50		CCT GAT GAT GAA CCA GTG GCC GAT CCT TAT GAT CAG TCC TTT GAA AGC Pro Asp Asp Glu Pro Val Ala Asp Pro Tyr Asp Gln Ser Phe Glu Ser	1728			
		565	570	575		
55		AGG GAC CTC CTT ATA GAT GAG TGG AAA AGC CTG ACC TAT GAT GAA GTC Arg Asp Leu Leu Ile Asp Glu Trp Lys Ser Leu Thr Tyr Asp Glu Val	1776			
		580	585	590		
60		ATC AGC TTT GTG CCA CCA CCC CTT GAC CAA GAA GAG ATG GAG TCC TGA Ile Ser Phe Val Pro Pro Pro Leu Asp Gln Glu Glu Met Glu Ser	1824			
		595	600	605		

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 607 amino acids

(B) TYPE: amino acid

90

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

10 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
    1      5      10      15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
    20      25      30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
    35      40      45
15 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50      55      60
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
    65      70      75      80
20 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
    85      90      95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
    100      105      110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
    115      120      125
25 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130      135      140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
    145      150      155      160
30 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
    165      170      175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
    180      185      190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
    195      200      205
35 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    210      215      220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
    225      230      235      240
40 Gly Leu Arg Ser Arg Gly Lys Met Ser Gln Glu Arg Pro Thr Phe Tyr
    245      250      255
Arg Gln Glu Leu Asn Lys Thr Ile Trp Glu Val Pro Glu Arg Tyr Gln
    260      265      270
Asn Leu Ser Pro Val Gly Ser Gly Ala Tyr Gly Ser Val Cys Ala Ala
    275      280      285
45 Phe Asp Thr Lys Thr Gly Leu Arg Val Ala Val Lys Lys Leu Ser Arg
    290      295      300
Pro Phe Gln Ser Ile Ile His Ala Lys Arg Thr Tyr Arg Glu Leu Arg
    305      310      315      320
50 Leu Leu Lys His Met Lys His Glu Asn Val Ile Gly Leu Leu Asp Val
    325      330      335
Phe Thr Pro Ala Arg Ser Leu Glu Glu Phe Asn Asp Val Tyr Leu Val
    340      345      350
Thr His Leu Met Gly Ala Asp Leu Asn Asn Ile Val Lys Cys Gln Lys
    355      360      365
55 Leu Thr Asp Asp His Val Gln Phe Leu Ile Tyr Gln Ile Leu Arg Gly
    370      375      380

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90

91

Leu Lys Tyr Ile His Ser Ala Asp Ile Ile His Arg Asp Leu Lys Pro  
 385 390 395 400  
 Ser Asn Leu Ala Val Asn Glu Asp Cys Glu Leu Lys Ile Leu Asp Phe  
 405 410 415  
 5 Gly Leu Ala Arg His Thr Asp Asp Glu Met Thr Gly Tyr Val Ala Thr  
 420 425 430  
 Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Trp Met His Tyr Asn  
 435 440 445  
 10 Gln Thr Val Asp Ile Trp Ser Val Gly Cys Ile Met Ala Glu Leu Leu  
 450 455 460  
 Thr Gly Arg Thr Leu Phe Pro Gly Thr Asp His Ile Asp Gln Leu Lys  
 465 470 475 480  
 Leu Ile Leu Arg Leu Val Gly Thr Pro Gly Ala Glu Leu Leu Lys Lys  
 485 490 495  
 15 Ile Ser Ser Glu Ser Ala Arg Asn Tyr Ile Gln Ser Leu Thr Gln Met  
 500 505 510  
 Pro Lys Met Asn Phe Ala Asn Val Phe Ile Gly Ala Asn Pro Leu Ala  
 515 520 525  
 20 Val Asp Leu Leu Glu Lys Met Leu Val Leu Asp Ser Asp Lys Arg Ile  
 530 535 540  
 Thr Ala Ala Gln Ala Leu Ala His Ala Tyr Phe Ala Gln Tyr His Asp  
 545 550 555 560  
 Pro Asp Asp Glu Pro Val Ala Asp Pro Tyr Asp Gln Ser Phe Glu Ser  
 565 570 575  
 25 Arg Asp Leu Leu Ile Asp Glu Trp Lys Ser Leu Thr Tyr Asp Glu Val  
 580 585 590  
 Ile Ser Phe Val Pro Pro Pro Leu Asp Gln Glu Glu Met Glu Ser  
 595 600 605

30 (2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2907 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

40 (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...2904  
 (D) OTHER INFORMATION:

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 50 GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 55 GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

91

92

	35	40	45	
5	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60	192		
10	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 65 70 75 80	240		
	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95	288		
15	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110	336		
20	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125	384		
25	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGC CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140	432		
30	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160	480		
	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175	528		
35	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190	576		
40	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205	624		
45	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220	672		
50	GTG ACC GCC GCC GGC ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser 225 230 235 240	720		
	GGA CTC AGA TCT ATG AGT GCT GAG GGC TAC CAG TAC AGA GCG CTG TAT Gly Leu Arg Ser Met Ser Ala Glu Gly Tyr Gln Tyr Arg Ala Leu Tyr 245 250 255	768		
55	GAT TAT AAA AAG GAA AGA GAA GAA GAT ATT GAC TTG CAC TTG GGT GAC Asp Tyr Lys Lys Glu Arg Glu Glu Asp Ile Asp Leu His Leu Gly Asp	816		

92



93

	260	265	270	
5	ATA TTG ACT GTG AAT AAA GGG TCC TTA GTA GCT CTT GGA TTC AGT GAT Ile Leu Thr Val Asn Lys Gly Ser Leu Val Ala Leu Gly Phe Ser Asp 275 280 285	864		
10	GGA CAG GAA GCC AGG CCT GAA GAA ATT GGC TGG TTA AAT GGC TAT AAT Gly Gln Glu Ala Arg Pro Glu Glu Ile Gly Trp Leu Asn Gly Tyr Asn 290 295 300	912		
15	GAA ACC ACA GGG GAA AGG GGG GAC TTT CCG GGA ACT TAC GTA GAA TAT Glu Thr Thr Gly Glu Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Tyr 305 310 315 320	960		
20	ATT GGA AGG AAA AAA ATC TCG CCT CCC ACA CCA AAG CCC CGG CCA CCT Ile Gly Arg Lys Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro 325 330 335	1008		
25	CGG CCT CTT CCT GTT GCA CCA GGT TCT TCG AAA ACT GAA GCA GAT GTT Arg Pro Leu Pro Val Ala Pro Gly Ser Ser Lys Thr Glu Ala Asp Val 340 345 350	1056		
30	GAA CAA CAA GCT TTG ACT CTC CCG GAT CTT GCA GAG CAG TTT GCC CCT Glu Gln Gln Ala Leu Thr Leu Pro Asp Leu Ala Glu Gln Phe Ala Pro 355 360 365	1104		
35	CCT GAC ATT GCC CCG CCT CTT CTT ATC AAG CTC GTG GAA GCC ATT GAA Pro Asp Ile Ala Pro Pro Leu Leu Ile Lys Leu Val Glu Ala Ile Glu 370 375 380	1152		
40	AAG AAA GGT CTG GAA TGT TCA ACT CTA TAC AGA ACA CAG AGC TCC AGC Lys Lys Gly Leu Glu Cys Ser Thr Leu Tyr Arg Thr Gln Ser Ser Ser 385 390 395 400	1200		
45	AAC CTG GCA GAA TTA CGA CAG CTT CTT GAT TGT GAT ACA CCC TCC GTG Asn Leu Ala Glu Leu Arg Gln Leu Leu Asp Cys Asp Thr Pro Ser Val 405 410 415	1248		
50	GAC TTG GAA ATG ATC GAT GTG CAC GTT TTG GCT GAC GCT TTC AAA CGC Asp Leu Glu Met Ile Asp Val His Val Leu Ala Asp Ala Phe Lys Arg 420 425 430	1296		
55	TAT CTC CTG GAC TTA CCA AAT CCT GTC ATT CCA GCA GCC GTT TAC AGT Tyr Leu Leu Asp Leu Pro Asn Pro Val Ile Pro Ala Ala Val Tyr Ser 435 440 445	1344		
60	GAA ATG ATT TCT TTA GCT CCA GAA GTA CAA AGC TCC GAA GAA TAT ATT Glu Met Ile Ser Leu Ala Pro Glu Val Gln Ser Ser Glu Glu Tyr Ile 450 455 460	1392		
65	CAG CTA TTG AAG AAG CTT ATT AGG TCG CCT AGC ATA CCT CAT CAG TAT Gln Leu Leu Lys Lys Leu Ile Arg Ser Pro Ser Ile Pro His Gln Tyr 465 470 475 480	1440		
70	TGG CTT ACG CTT CAG TAT TTG TTA AAA CAT TTC TTC AAG CTC TCT CAA Trp Leu Thr Leu Gln Tyr Leu Leu Lys His Phe Phe Lys Leu Ser Gln	1488		

93



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	705	710	715	720	
5	ATC CAA ATG AAA AGG ACA GCT ATT GAA GCA TTT AAT GAA ACC ATA AAA Ile Gln Met Lys Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys	725	730	735	2208
10	ATA TTT GAA GAA CAG TGC CAG ACC CAA GAG CGG TAC AGC AAA GAA TAC Ile Phe Glu Glu Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr	740	745	750	2256
15	ATA GAA AAG TTT AAA CGT GAA GGC AAT GAG AAA GAA ATA CAA AGG ATT Ile Glu Lys Phe Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile	755	760	765	2304
20	ATG CAT AAT TAT GAT AAG TTG AAG TCT CGA ATC AGT GAA ATT ATT GAC Met His Asn Tyr Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp	770	775	780	2352
25	AGT AGA AGA AGA TTG GAA GAA GAC TTG AAG AAG CAG GCA GCT GAG TAT Ser Arg Arg Arg Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr	785	790	795	2400
30	CGA GAA ATT GAC AAA CGT ATG AAC AGC ATT AAA CCA GAC CTT ATC CAG Arg Glu Ile Asp Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln	805	810	815	2448
35	CTG AGA AAG ACG AGA GAC CAA TAC TTG ATG TGG TTG ACT CAA AAA GGT Leu Arg Lys Thr Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly	820	825	830	2496
40	GTT CGG CAA AAG AAG TTG AAC GAG TGG TTG GGC AAT GAA AAC ACT GAA Val Arg Gln Lys Lys Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu	835	840	845	2544
45	GAC CAA TAT TCA CTG GTG GAA GAT GAT GAA GAT TTG CCC CAT CAT GAT Asp Gln Tyr Ser Leu Val Glu Asp Asp Glu Asp Leu Pro His His Asp	850	855	860	2592
50	GAG AAG ACA TGG AAT GTT GGA AGC AGC AAC CGA AAC AAA GCT GAA AAC Glu Lys Thr Trp Asn Val Gly Ser Ser Asn Arg Asn Lys Ala Glu Asn	865	870	875	2640
55	CTG TTG CGA GGG AAG CGA GAT GGC ACT TTT CTT GTC CGG GAG AGC AGT Leu Leu Arg Gly Lys Arg Asp Gly Thr Phe Leu Val Arg Glu Ser Ser	885	890	895	2688
60	AAA CAG GGC TGC TAT GCC TGC TCT GTA GTG GTG GAC GGC GAA GTA AAG Lys Gln Gly Cys Tyr Ala Cys Ser Val Val Val Asp Gly Glu Val Lys	900	905	910	2736
65	CAT TGT GTC ATA AAC AAA ACA GCA ACT GGC TAT GGC TTT GCC GAG CCC His Cys Val Ile Asn Lys Thr Ala Thr Gly Tyr Gly Phe Ala Glu Pro	915	920	925	2784
70	TAT AAC TTG TAC AGC TCT CTG AAA GAA CTG GTG CTA CAT TAC CAA CAC Tyr Asn Leu Tyr Ser Ser Leu Lys Glu Leu Val Leu His Tyr Gln His				2832

95

96

930 935 940

ACC TCC CTT GTG CAG CAC AAC GAC TCC CTC AAT GTC ACA CTA GCC TAC 2880  
 Thr Ser Leu Val Gln His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr  
 5 945 950 955 960

CCA GTA TAT GCA CAG CAG AGG CGA TGA 2907  
 Pro Val Tyr Ala Gln Gln Arg Arg  
 965

10

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 968 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

25 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 30 35 40 45  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 35 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 40 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
 45 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190  
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
 195 200 205  
 50 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220  
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser  
 225 230 235 240  
 55 Gly Leu Arg Ser Met Ser Ala Glu Gly Tyr Gln Tyr Arg Ala Leu Tyr  
 245 250 255

96

97

	Asp	Tyr	Lys	Lys	Glu	Arg	Glu	Glu	Asp	Ile	Asp	Leu	His	Leu	Gly	Asp
				260					265					270		
	Ile	Leu	Thr	Val	Asn	Lys	Gly	Ser	Leu	Val	Ala	Leu	Gly	Phe	Ser	Asp
			275					280					285			
5	Gly	Gln	Glu	Ala	Arg	Pro	Glu	Glu	Ile	Gly	Trp	Leu	Asn	Gly	Tyr	Asn
		290					295					300				
	Glu	Thr	Thr	Gly	Glu	Arg	Gly	Asp	Phe	Pro	Gly	Thr	Tyr	Val	Glu	Tyr
	305				310					315					320	
	Ile	Gly	Arg	Lys	Lys	Ile	Ser	Pro	Pro	Thr	Pro	Lys	Pro	Arg	Pro	Pro
10				325						330				335		
	Arg	Pro	Leu	Pro	Val	Ala	Pro	Gly	Ser	Ser	Lys	Thr	Glu	Ala	Asp	Val
			340					345				350				
	Glu	Gln	Gln	Ala	Leu	Thr	Leu	Pro	Asp	Leu	Ala	Glu	Gln	Phe	Ala	Pro
		355						360				365				
15	Pro	Asp	Ile	Ala	Pro	Pro	Leu	Leu	Ile	Lys	Leu	Val	Glu	Ala	Ile	Glu
		370					375					380				
	Lys	Lys	Gly	Leu	Glu	Cys	Ser	Thr	Leu	Tyr	Arg	Thr	Gln	Ser	Ser	Ser
	385				390					395						400
	Asn	Leu	Ala	Glu	Leu	Arg	Gln	Leu	Leu	Asp	Cys	Asp	Thr	Pro	Ser	Val
20				405						410				415		
	Asp	Leu	Glu	Met	Ile	Asp	Val	His	Val	Leu	Ala	Asp	Ala	Phe	Lys	Arg
			420					425					430			
	Tyr	Leu	Leu	Asp	Leu	Pro	Asn	Pro	Val	Ile	Pro	Ala	Ala	Val	Tyr	Ser
		435					440					445				
25	Glu	Met	Ile	Ser	Leu	Ala	Pro	Glu	Val	Gln	Ser	Ser	Glu	Glu	Tyr	Ile
		450					455					460				
	Gln	Leu	Leu	Lys	Lys	Leu	Ile	Arg	Ser	Pro	Ser	Ile	Pro	His	Gln	Tyr
	465				470					475					480	
	Trp	Leu	Thr	Leu	Gln	Tyr	Leu	Leu	Lys	His	Phe	Phe	Lys	Leu	Ser	Gln
30				485						490				495		
	Thr	Ser	Ser	Lys	Asn	Leu	Leu	Asn	Ala	Arg	Val	Leu	Ser	Glu	Ile	Phe
			500					505					510			
	Ser	Pro	Met	Leu	Phe	Arg	Phe	Ser	Ala	Ala	Ser	Ser	Asp	Asn	Thr	Glu
		515					520					525				
35	Asn	Leu	Ile	Lys	Val	Ile	Glu	Ile	Leu	Ile	Ser	Thr	Glu	Trp	Asn	Glu
		530					535					540				
	Arg	Gln	Pro	Ala	Pro	Ala	Leu	Pro	Pro	Lys	Pro	Pro	Lys	Pro	Thr	Thr
	545				550					555					560	
	Val	Ala	Asn	Asn	Gly	Met	Asn	Asn	Asn	Met	Ser	Leu	Gln	Asn	Ala	Glu
40				565						570				575		
	Trp	Tyr	Trp	Gly	Asp	Ile	Ser	Arg	Glu	Glu	Val	Asn	Glu	Lys	Leu	Arg
			580					585				590				
	Asp	Thr	Ala	Asp	Gly	Thr	Phe	Leu	Val	Arg	Asp	Ala	Ser	Thr	Lys	Met
		595					600					605				
45	His	Gly	Asp	Tyr	Thr	Leu	Thr	Leu	Arg	Lys	Gly	Gly	Asn	Asn	Lys	Leu
		610					615					620				
	Ile	Lys	Ile	Phe	His	Arg	Asp	Gly	Lys	Tyr	Gly	Phe	Ser	Asp	Pro	Leu
	625				630					635					640	
	Thr	Phe	Ser	Ser	Val	Val	Glu	Leu	Ile	Asn	His	Tyr	Arg	Asn	Glu	Ser
50				645						650				655		
	Leu	Ala	Gln	Tyr	Asn	Pro	Lys	Leu	Asp	Val	Lys	Leu	Leu	Tyr	Pro	Val
		660						665				670				
	Ser	Lys	Tyr	Gln	Gln	Asp	Gln	Val	Lys	Glu	Asp	Asn	Ile	Glu	Ala	
		675					680					685				
55	Val	Gly	Lys	Lys	Leu	His	Glu	Tyr	Asn	Thr	Gln	Phe	Gln	Glu	Lys	Ser
		690					695					700				

97

98

Arg Glu Tyr Asp Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu  
 705 710 715 720  
 Ile Gln Met Lys Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys  
 725 730 735  
 5 Ile Phe Glu Glu Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr  
 740 745 750  
 Ile Glu Lys Phe Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile  
 755 760 765  
 10 Met His Asn Tyr Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp  
 770 775 780  
 Ser Arg Arg Arg Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr  
 785 790 795 800  
 Arg Glu Ile Asp Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln  
 805 810 815  
 15 Leu Arg Lys Thr Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly  
 820 825 830  
 Val Arg Gln Lys Lys Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu  
 835 840 845  
 Asp Gln Tyr Ser Leu Val Glu Asp Asp Glu Asp Leu Pro His His Asp  
 850 855 860  
 20 Glu Lys Thr Trp Asn Val Gly Ser Ser Asn Arg Asn Lys Ala Glu Asn  
 865 870 875 880  
 Leu Leu Arg Gly Lys Arg Asp Gly Thr Phe Leu Val Arg Glu Ser Ser  
 885 890 895  
 25 Lys Gln Gly Cys Tyr Ala Cys Ser Val Val Val Asp Gly Glu Val Lys  
 900 905 910  
 His Cys Val Ile Asn Lys Thr Ala Thr Gly Tyr Gly Phe Ala Glu Pro  
 915 920 925  
 Tyr Asn Leu Tyr Ser Ser Leu Lys Glu Leu Val Leu His Tyr Gln His  
 930 935 940  
 30 Thr Ser Leu Val Gln His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr  
 945 950 955 960  
 Pro Val Tyr Ala Gln Gln Arg Arg  
 965

35

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 2160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...2157  
 (D) OTHER INFORMATION:

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

55

48

98

99

	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
5	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
10	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Thr Leu Val Thr Thr	
	50 55 60	
15	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
20	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
25	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
30	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
35	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
40	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
45	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
50	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC	576
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
55	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG	624
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
	195 200 205	
60	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC	672
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
	210 215 220	
65	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC	720
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	

100																	
	GGA	CTC	AGA	TCT	CGA	GCT	CAA	GCT	TCG	AAT	TCG	ACC	ATG	TCG	TCC	ATC	768
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Thr	Met	Ser	Ser	Ile	
					245					250					255		
5	TTG	CCA	TTC	ACG	CCG	CCA	GTT	GTG	AAG	AGA	CTG	CTG	GGA	TGG	AAG	AAG	816
	Leu	Pro	Phe	Thr	Pro	Pro	Val	Val	Lys	Arg	Leu	Leu	Gly	Trp	Lys	Lys	
				260					265					270			
10	TCA	GCT	GGT	GGG	TCT	GGA	GGA	GCA	GGC	GGA	GGA	GAG	CAG	AAT	GGG	CAG	864
	Ser	Ala	Gly	Gly	Ser	Gly	Gly	Ala	Gly	Gly	Gly	Glu	Gln	Asn	Gly	Gln	
			275					280					285				
15	GAA	GAA	AAG	TGG	TGT	GAG	AAA	GCA	GTG	AAA	AGT	CTG	GTG	AAG	AAG	CTA	912
	Glu	Glu	Lys	Trp	Cys	Glu	Lys	Ala	Val	Lys	Ser	Leu	Val	Lys	Lys	Leu	
		290					295					300					
20	AAG	AAA	ACA	GGA	CGA	TTA	GAT	GAG	CTT	GAG	AAA	GCC	ATC	ACC	ACT	CAA	960
	Lys	Lys	Thr	Gly	Arg	Leu	Asp	Glu	Leu	Glu	Lys	Ala	Ile	Thr	Thr	Gln	
	305					310					315					320	
25	AAC	TGT	AAT	ACT	AAA	TGT	GTT	ACC	ATA	CCA	AGC	ACT	TGC	TCT	GAA	ATT	1008
	Asn	Cys	Asn	Thr	Lys	Cys	Val	Thr	Ile	Pro	Ser	Thr	Cys	Ser	Glu	Ile	
					325					330					335		
30	TGG	GGA	CTG	AGT	ACA	CCA	AAT	ACG	ATA	GAT	CAG	TGG	GAT	ACA	ACA	GGC	1056
	Trp	Gly	Leu	Ser	Thr	Pro	Asn	Thr	Ile	Asp	Gln	Trp	Asp	Thr	Thr	Gly	
				340					345					350			
35	CTT	TAC	AGC	TTC	TCT	GAA	CAA	ACC	AGG	TCT	CTT	GAT	GGT	CGT	CTC	CAG	1104
	Leu	Tyr	Ser	Phe	Ser	Glu	Gln	Thr	Arg	Ser	Leu	Asp	Gly	Arg	Leu	Gln	
			355					360					365				
40	GTA	TCC	CAT	CGA	AAA	GGA	TTG	CCA	CAT	GTT	ATA	TAT	TGC	CGA	TTA	TGG	1152
	Val	Ser	His	Arg	Lys	Gly	Leu	Pro	His	Val	Ile	Tyr	Cys	Arg	Leu	Trp	
		370					375					380					
45	CGC	TGG	CCT	GAT	CTT	CAC	AGT	CAT	CAT	GAA	CTC	AAG	GCA	ATT	GAA	AAC	1200
	Arg	Trp	Pro	Asp	Leu	His	Ser	His	His	Glu	Leu	Lys	Ala	Ile	Glu	Asn	
	385					390					395					400	
50	TGC	GAA	TAT	GCT	TTT	AAT	CTT	AAA	AAG	GAT	GAA	GTA	TGT	GTA	AAC	CCT	1248
	Cys	Glu	Tyr	Ala	Phe	Asn	Leu	Lys	Lys	Asp	Glu	Val	Cys	Val	Asn	Pro	
				405						410					415		
55	TAC	CAC	TAT	CAG	AGA	GTT	GAG	ACA	CCA	GTT	TTG	CCT	CCA	GTA	TTA	GTG	1296
	Tyr	His	Tyr	Gln	Arg	Val	Glu	Thr	Pro	Val	Leu	Pro	Pro	Val	Leu	Val	
				420					425					430			
60	CCC	CGA	CAC	ACC	GAG	ATC	CTA	ACA	GAA	CTT	CCG	CCT	CTG	GAT	GAC	TAT	1344
	Pro	Arg	His	Thr	Glu	Ile	Leu	Thr	Glu	Leu	Pro	Pro	Leu	Asp	Asp	Tyr	
			435					440					445				
65	ACT	CAC	TCC	ATT	CCA	GAA	AAC	ACT	AAC	TTC	CCA	GCA	GGA	ATT	GAG	CCA	1392
	Thr	His	Ser	Ile	Pro	Glu	Asn	Thr	Asn	Phe	Pro	Ala	Gly	Ile	Glu	Pro	
		450					455					460					



101

	CAG AGT AAT TAT ATT CCA GAA ACG CCA CCT CCT GGA TAT ATC AGT GAA	1440
	Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly Tyr Ile Ser Glu	
	465 470 475 480	
5	GAT GGA GAA ACA AGT GAC CAA CAG TTG AAT CAA AGT ATG GAC ACA GGC	1488
	Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser Met Asp Thr Gly	
	485 490 495	
10	TCT CCA GCA GAA CTA TCT CCT ACT ACT CTT TCC CCT GTT AAT CAT AGC	1536
	Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro Val Asn His Ser	
	500 505 510	
	TTG GAT TTA CAG CCA GTT ACT TAC TCA GAA CCT GCA TTT TGG TGT TCA	1584
15	Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala Phe Trp Cys Ser	
	515 520 525	
	ATA GCA TAT TAT GAA TTA AAT CAG AGG GTT GGA GAA ACC TTC CAT GCA	1632
	Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr Phe His Ala	
	530 535 540	
20	TCA CAG CCC TCA CTC ACT GTA GAT GGC TTT ACA GAC CCA TCA AAT TCA	1680
	Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro Ser Asn Ser	
	545 550 555 560	
25	GAG AGG TTC TGC TTA GGT TTA CTC TCC AAT GTT AAC CGA AAT GCC ACG	1728
	Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg Asn Ala Thr	
	565 570 575	
30	GTA GAA ATG ACA AGA AGG CAT ATA GGA AGA GGA GTG CGC TTA TAC TAC	1776
	Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr	
	580 585 590	
	ATA GGT GGG GAA GTT TTT GCT GAG TGC CTA AGT GAT AGT GCA ATC TTT	1824
35	Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe	
	595 600 605	
	GTG CAG AGC CCC AAT TGT AAT CAG AGA TAT GGC TGG CAC CCT GCA ACA	1872
	Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His Pro Ala Thr	
	610 615 620	
40	GTG TGT AAA ATT CCA CCA GGC TGT AAT CTG AAG ATC TTC AAC AAC CAG	1920
	Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe Asn Asn Gln	
	625 630 635 640	
45	GAA TTT GCT GCT CTT CTG GCT CAG TCT GTT AAT CAG GGT TTT GAA GCC	1968
	Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly Phe Glu Ala	
	645 650 655	
50	GTC TAT CAG CTA ACT AGA ATG TGC ACC ATA AGA ATG AGT TTT GTG AAA	2016
	Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser Phe Val Lys	
	660 665 670	
55	GGG TGG GGA GCA GAA TAC CGA AGG CAG ACG GTA ACA AGT ACT CCT TGC	2064
	Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser Thr Pro Cys	
	675 680 685	

102

TGG ATT GAA CTT CAT CTG AAT GGA CCT CTA CAG TGG TTG GAC AAA GTA 2112  
 Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu Asp Lys Val  
 690 695 700

5 TTA ACT CAG ATG GGA TCC CCT TCA GTG CGT TGC TCA AGC ATG TCA TAA 2160  
 Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser Met Ser  
 705 710 715

10 (2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 amino acids

(B) TYPE: amino acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 25 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 30 50 55 60  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 35 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 40 130 135 140  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175  
 45 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190  
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
 195 200 205  
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 50 210 215 220  
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser  
 225 230 235 240  
 Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Ser Ser Ile  
 245 250 255  
 55 Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu Gly Trp Lys Lys  
 260 265 270

102

103

Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu Gln Asn Gly Gln  
 275 280 285  
 Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu Val Lys Lys Leu  
 290 295 300  
 5 Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln  
 305 310 315 320  
 Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr Cys Ser Glu Ile  
 325 330 335  
 10 Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp Asp Thr Thr Gly  
 340 345 350  
 Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp Gly Arg Leu Gln  
 355 360 365  
 Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr Cys Arg Leu Trp  
 370 375 380  
 15 Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys Ala Ile Glu Asn  
 385 390 395 400  
 Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val Cys Val Asn Pro  
 405 410 415  
 20 Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro Pro Val Leu Val  
 420 425 430  
 Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro Leu Asp Asp Tyr  
 435 440 445  
 Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro  
 450 455 460  
 25 Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly Tyr Ile Ser Glu  
 465 470 475 480  
 Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser Met Asp Thr Gly  
 485 490 495  
 30 Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro Val Asn His Ser  
 500 505 510  
 Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala Phe Trp Cys Ser  
 515 520 525  
 Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr Phe His Ala  
 530 535 540  
 35 Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro Ser Asn Ser  
 545 550 555 560  
 Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg Asn Ala Thr  
 565 570 575  
 40 Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr  
 580 585 590  
 Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe  
 595 600 605  
 Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His Pro Ala Thr  
 610 615 620  
 45 Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe Asn Asn Gln  
 625 630 635 640  
 Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly Phe Glu Ala  
 645 650 655  
 50 Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser Phe Val Lys  
 660 665 670  
 Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser Thr Pro Cys  
 675 680 685  
 Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu Asp Lys Val  
 690 695 700  
 55 Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser Met Ser  
 705 710 715

103

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2421 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2418

15 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

20	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
25	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
30	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
35	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
40	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
45	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
50	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
55	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
60	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGC CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
65	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	

105																	
145	150						155						160				
5	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
	165						170						175				
10	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
	180						185						190				
15	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
	195						200						205				
20	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
	210						215						220				
25	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225						230						235				
30	GGA	CTC	AGA	TCT	CGA	GCT	CAA	GCT	TCG	AAT	TCG	AAT	TCA	ACC	ATG	GAC	768
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Asn	Ser	Thr	Met	Asp	
	245						250						255				
35	AAT	ATG	TCT	ATT	ACG	AAT	ACA	CCA	ACA	AGT	AAT	GAT	GCC	TGT	CTG	AGC	816
	Asn	Met	Ser	Ile	Thr	Asn	Thr	Pro	Thr	Ser	Asn	Asp	Ala	Cys	Leu	Ser	
	260						265						270				
40	ATT	GTG	CAT	AGT	TTG	ATG	TGC	CAT	AGA	CAA	GGT	GGA	GAG	AGT	GAA	ACA	864
	Ile	Val	His	Ser	Leu	Met	Cys	His	Arg	Gln	Gly	Gly	Glu	Ser	Glu	Thr	
	275						280						285				
45	TTT	GCA	AAA	AGA	GCA	ATT	GAA	AGT	TTG	GTA	AAG	AAG	CTG	AAG	GAG	AAA	912
	Phe	Ala	Lys	Arg	Ala	Ile	Glu	Ser	Leu	Val	Lys	Lys	Leu	Lys	Glu	Lys	
	290						295						300				
50	AAA	GAT	GAA	TTG	GAT	TCT	TTA	ATA	ACA	GCT	ATA	ACT	ACA	AAT	GGA	GCT	960
	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Ile	Thr	Ala	Ile	Thr	Thr	Asn	Gly	Ala	
	305						310						315				
55	CAT	CCT	AGT	AAA	TGT	GTT	ACC	ATA	CAG	AGA	ACA	TTG	GAT	GGG	AGG	CTT	1008
	His	Pro	Ser	Lys	Cys	Val	Thr	Ile	Gln	Arg	Thr	Leu	Asp	Gly	Arg	Leu	
	325						330						335				
60	CAG	GTG	GCT	GGT	CGG	AAA	GGA	TTT	CCT	CAT	GTG	ATC	TAT	GCC	CGT	CTC	1056
	Gln	Val	Ala	Gly	Arg	Lys	Gly	Phe	Pro	His	Val	Ile	Tyr	Ala	Arg	Leu	
	340						345						350				
65	TGG	AGG	TGG	CCT	GAT	CTT	CAC	AAA	AAT	GAA	CTA	AAA	CAT	GTT	AAA	TAT	1104
	Trp	Arg	Trp	Pro	Asp	Leu	His	Lys	Asn	Glu	Leu	Lys	His	Val	Lys	Tyr	
	355						360						365				
70	TGT	CAG	TAT	GCG	TTT	GAC	TTA	AAA	TGT	GAT	AGT	GTC	TGT	GTG	AAT	CCA	1152
	Cys	Gln	Tyr	Ala	Phe	Asp	Leu	Lys	Cys	Asp	Ser	Val	Cys	Val	Asn	Pro	

106

	370	375	380	
5	TAT CAC TAC GAA CGA GTT GTA TCA CCT GGA ATT GAT CTC TCA GGA TTA Tyr His Tyr Glu Arg Val Val Ser Pro Gly Ile Asp Leu Ser Gly Leu 385 390 395 400	1200		
10	ACA CTG CAG AGT AAT GCT CCA TCA AGT ATG ATG GTG AAG GAT GAA TAT Thr Leu Gln Ser Asn Ala Pro Ser Ser Met Met Val Lys Asp Glu Tyr 405 410 415	1248		
15	GTG CAT GAC TTT GAG GGA CAG CCA TCG TTG TCC ACT GAA GGA CAT TCA Val His Asp Phe Glu Gly Gln Pro Ser Leu Ser Thr Glu Gly His Ser 420 425 430	1296		
20	ATT CAA ACC ATC CAG CAT CCA CCA AGT AAT CGT GCA TCG ACA GAG ACA Ile Gln Thr Ile Gln His Pro Pro Ser Asn Arg Ala Ser Thr Glu Thr 435 440 445	1344		
25	TAC AGC ACC CCA GCT CTG TTA GCC CCA TCT GAG TCT AAT GCT ACC AGC Tyr Ser Thr Pro Ala Leu Leu Ala Pro Ser Glu Ser Asn Ala Thr Ser 450 455 460	1392		
30	ACT GCC AAC TTT CCC AAC ATT CCT GTG GCT TCC ACA AGT CAG CCT GCC Thr Ala Asn Phe Pro Asn Ile Pro Val Ala Ser Thr Ser Gln Pro Ala 465 470 475 480	1440		
35	AGT ATA CTG GGG GGC AGC CAT AGT GAA GGA CTG TTG CAG ATA GCA TCA Ser Ile Leu Gly Gly Ser His Ser Glu Gly Leu Leu Gln Ile Ala Ser 485 490 495	1488		
40	GGG CCT CAG CCA GGA CAG CAG CAG AAT GGA TTT ACT GGT CAG CCA GCT Gly Pro Gln Pro Gly Gln Gln Gln Asn Gly Phe Thr Gly Gln Pro Ala 500 505 510	1536		
45	ACT TAC CAT CAT AAC AGC ACT ACC ACC TGG ACT GGA AGT AGG ACT GCA Thr Tyr His His Asn Ser Thr Thr Thr Trp Thr Gly Ser Arg Thr Ala 515 520 525	1584		
50	CCA TAC ACA CCT AAT TTG CCT CAC CAC CAA AAC GGC CAT CTT CAG CAC Pro Tyr Thr Pro Asn Leu Pro His His Gln Asn Gly His Leu Gln His 530 535 540	1632		
55	CAC CCG CCT ATG CCG CCC CAT CCC GGA CAT TAC TGG CCT GTT CAC AAT His Pro Pro Met Pro Pro His Pro Gly His Tyr Trp Pro Val His Asn 545 550 555 560	1680		
60	GAG CTT GCA TTC CAG CCT CCC ATT TCC AAT CAT CCT GCT CCT GAG TAT Glu Leu Ala Phe Gln Pro Pro Ile Ser Asn His Pro Ala Pro Glu Tyr 565 570 575	1728		
65	TGG TGT TCC ATT GCT TAC TTT GAA ATG GAT GTT CAG GTA GGA GAG ACA Trp Cys Ser Ile Ala Tyr Phe Glu Met Asp Val Gln Val Gly Glu Thr 580 585 590	1776		
70	TTT AAG GTT CCT TCA AGC TGC CCT ATT GTT ACT GTT GAT GGA TAC GTG Phe Lys Val Pro Ser Ser Cys Pro Ile Val Thr Val Asp Gly Tyr Val 600 605 610 615	1824		

106

107																		
595					600					605								
5	GAC	CCT	TCT	GGA	GGA	GAT	CGC	TTT	TGT	TTG	GGT	CAA	CTC	TCC	AAT	GTC	1872	
	Asp	Pro	Ser	Gly	Gly	Asp	Arg	Phe	Cys	Leu	Gly	Gln	Leu	Ser	Asn	Val		
	610				615				620									
10	CAC	AGG	ACA	GAA	GCC	ATT	GAG	AGA	GCA	AGG	TTG	CAC	ATA	GGC	AAA	GGT	1920	
	His	Arg	Thr	Glu	Ala	Ile	Glu	Arg	Ala	Arg	Leu	His	Ile	Gly	Lys	Gly		
	625				630				635				640					
15	GTG	CAG	TTG	GAA	TGT	AAA	GGT	GAA	GGT	GAT	GTT	TGG	GTC	AGG	TGC	CTT	1968	
	Val	Gln	Leu	Glu	Cys	Lys	Gly	Glu	Gly	Asp	Val	Trp	Val	Arg	Cys	Leu		
	645				650				655									
20	AGT	GAC	CAC	GCG	GTC	TTT	GTA	CAG	AGT	TAC	TAC	TTA	GAC	AGA	GAA	GCT	2016	
	Ser	Asp	His	Ala	Val	Phe	Val	Gln	Ser	Tyr	Tyr	Leu	Asp	Arg	Glu	Ala		
	660				665				670									
25	GGG	CGT	GCA	CCT	GGA	GAT	GCT	GTT	CAT	AAG	ATC	TAC	CCA	AGT	GCA	TAT	2064	
	Gly	Arg	Ala	Pro	Gly	Asp	Ala	Val	His	Lys	Ile	Tyr	Pro	Ser	Ala	Tyr		
	675				680				685									
30	ATA	AAG	GTC	TTT	GAT	TTG	CGT	CAG	TGT	CAT	CGA	CAG	ATG	CAG	CAG	CAG	2112	
	Ile	Lys	Val	Phe	Asp	Leu	Arg	Gln	Cys	His	Arg	Gln	Met	Gln	Gln	Gln		
	690				695				700									
35	GCG	GCT	ACT	GCA	CAA	GCT	GCA	GCA	GCT	GCC	CAG	GCA	GCA	GCC	GTG	GCA	2160	
	Ala	Ala	Thr	Ala	Gln	Ala	Ala	Ala	Ala	Ala	Gln	Ala	Ala	Ala	Val	Ala		
	705				710				715				720					
40	GGA	AAC	ATC	CCT	GGC	CCA	GGA	TCA	GTA	GGT	GGA	ATA	GCT	CCA	GCT	ATC	2208	
	Gly	Asn	Ile	Pro	Gly	Pro	Gly	Ser	Val	Gly	Gly	Ile	Ala	Pro	Ala	Ile		
	725				730				735									
45	AGT	CTG	TCA	GCT	GCT	GCT	GGA	ATT	GGT	GTT	GAT	GAC	CTT	CGT	CGC	TTA	2256	
	Ser	Leu	Ser	Ala	Ala	Ala	Gly	Ile	Gly	Val	Asp	Asp	Leu	Arg	Arg	Leu		
	740				745				750									
50	TGC	ATA	CTC	AGG	ATG	AGT	TTT	GTG	AAA	GGC	TGG	GGA	CCG	GAT	TAC	CCA	2304	
	Cys	Ile	Leu	Arg	Met	Ser	Phe	Val	Lys	Gly	Trp	Gly	Pro	Asp	Tyr	Pro		
	755				760				765									
55	AGA	CAG	AGC	ATC	AAA	GAA	ACA	CCT	TGC	TGG	ATT	GAA	ATT	CAC	TTA	CAC	2352	
	Arg	Gln	Ser	Ile	Lys	Glu	Thr	Pro	Cys	Trp	Ile	Glu	Ile	His	Leu	His		
	770				775				780									
60	CGG	GCC	CTC	CAG	CTC	CTA	GAC	GAA	GTA	CTT	CAT	ACC	ATG	CCG	ATT	GCA	2400	
	Arg	Ala	Leu	Gln	Leu	Leu	Asp	Glu	Val	Leu	His	Thr	Met	Pro	Ile	Ala		
	785				790				795				800					
65	GAC	CCA	CAA	CCT	TTA	GAC	TGA											2421
	Asp	Pro	Gln	Pro	Leu	Asp												
	805																	

(2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 806 amino acids

(B) TYPE: amino acid

5 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5				10					15			
15	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
				35				40					45				
20	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50						55					60					
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65				70						75				80		
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90					95			
25	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
				115				120					125				
30	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130						135					140					
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145				150						155				160		
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165					170					175			
35	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
				195			200						205				
40	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
	210						215					220					
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230					235				240		
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Asn	Ser	Thr	Met	Asp	
				245					250					255			
45	Asn	Met	Ser	Ile	Thr	Asn	Thr	Pro	Thr	Ser	Asn	Asp	Ala	Cys	Leu	Ser	
				260					265					270			
	Ile	Val	His	Ser	Leu	Met	Cys	His	Arg	Gln	Gly	Gly	Glu	Ser	Glu	Thr	
				275				280					285				
50	Phe	Ala	Lys	Arg	Ala	Ile	Glu	Ser	Leu	Val	Lys	Lys	Leu	Lys	Glu	Lys	
	290						295					300					
	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Ile	Thr	Ala	Ile	Thr	Thr	Asn	Gly	Ala	
	305					310					315				320		
	His	Pro	Ser	Lys	Cys	Val	Thr	Ile	Gln	Arg	Thr	Leu	Asp	Gly	Arg	Leu	
				325					330					335			
55	Gln	Val	Ala	Gly	Arg	Lys	Gly	Phe	Pro	His	Val	Ile	Tyr	Ala	Arg	Leu	
				340					345					350			



109

Trp Arg Trp Pro Asp Leu His Lys Asn Glu Leu Lys His Val Lys Tyr  
 355 360 365  
 Cys Gln Tyr Ala Phe Asp Leu Lys Cys Asp Ser Val Cys Val Asn Pro  
 370 375 380  
 5 Tyr His Tyr Glu Arg Val Val Ser Pro Gly Ile Asp Leu Ser Gly Leu  
 385 390 395 400  
 Thr Leu Gln Ser Asn Ala Pro Ser Ser Met Met Val Lys Asp Glu Tyr  
 405 410 415  
 10 Val His Asp Phe Glu Gly Gln Pro Ser Leu Ser Thr Glu Gly His Ser  
 420 425 430  
 Ile Gln Thr Ile Gln His Pro Pro Ser Asn Arg Ala Ser Thr Glu Thr  
 435 440 445  
 Tyr Ser Thr Pro Ala Leu Leu Ala Pro Ser Glu Ser Asn Ala Thr Ser  
 450 455 460  
 15 Thr Ala Asn Phe Pro Asn Ile Pro Val Ala Ser Thr Ser Gln Pro Ala  
 465 470 475 480  
 Ser Ile Leu Gly Gly Ser His Ser Glu Gly Leu Leu Gln Ile Ala Ser  
 485 490 495  
 20 Gly Pro Gln Pro Gly Gln Gln Gln Asn Gly Phe Thr Gly Gln Pro Ala  
 500 505 510  
 Thr Tyr His His Asn Ser Thr Thr Thr Trp Thr Gly Ser Arg Thr Ala  
 515 520 525  
 Pro Tyr Thr Pro Asn Leu Pro His His Gln Asn Gly His Leu Gln His  
 530 535 540  
 25 His Pro Pro Met Pro Pro His Pro Gly His Tyr Trp Pro Val His Asn  
 545 550 555 560  
 Glu Leu Ala Phe Gln Pro Pro Ile Ser Asn His Pro Ala Pro Glu Tyr  
 565 570 575  
 30 Trp Cys Ser Ile Ala Tyr Phe Glu Met Asp Val Gln Val Gly Glu Thr  
 580 585 590  
 Phe Lys Val Pro Ser Ser Cys Pro Ile Val Thr Val Asp Gly Tyr Val  
 595 600 605  
 Asp Pro Ser Gly Gly Asp Arg Phe Cys Leu Gly Gln Leu Ser Asn Val  
 610 615 620  
 35 His Arg Thr Glu Ala Ile Glu Arg Ala Arg Leu His Ile Gly Lys Gly  
 625 630 635 640  
 Val Gln Leu Glu Cys Lys Gly Glu Gly Asp Val Trp Val Arg Cys Leu  
 645 650 655  
 40 Ser Asp His Ala Val Phe Val Gln Ser Tyr Tyr Leu Asp Arg Glu Ala  
 660 665 670  
 Gly Arg Ala Pro Gly Asp Ala Val His Lys Ile Tyr Pro Ser Ala Tyr  
 675 680 685  
 Ile Lys Val Phe Asp Leu Arg Gln Cys His Arg Gln Met Gln Gln Gln  
 690 695 700  
 45 Ala Ala Thr Ala Gln Ala Ala Ala Ala Gln Ala Ala Val Ala  
 705 710 715 720  
 Gly Asn Ile Pro Gly Pro Gly Ser Val Gly Gly Ile Ala Pro Ala Ile  
 725 730 735  
 50 Ser Leu Ser Ala Ala Ala Gly Ile Gly Val Asp Asp Leu Arg Arg Leu  
 740 745 750  
 Cys Ile Leu Arg Met Ser Phe Val Lys Gly Trp Gly Pro Asp Tyr Pro  
 755 760 765  
 Arg Gln Ser Ile Lys Glu Thr Pro Cys Trp Ile Glu Ile His Leu His  
 770 775 780  
 55 Arg Ala Leu Gln Leu Leu Asp Glu Val Leu His Thr Met Pro Ile Ala  
 785 790 795 800

109

110

Asp Pro Gln Pro Leu Asp  
805

## (2) INFORMATION FOR SEQ ID NO:54:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

15

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...3117

(D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

20

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	

25

GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	

30

GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	

35

TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	

40

CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	

CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	

45

CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	

50

GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	

55

ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGC CAC AAG CTG GAG TAC	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	

110

111

	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
5	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
10	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC	576
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
15	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG	624
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
	195 200 205	
20	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC	672
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
	210 215 220	
25	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC	720
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	
30	GGA CTC AGA TCT ACC ATG GCG GGC TGG ATC CAG GCC CAG CAG CTG CAG	768
	Gly Leu Arg Ser Thr Met Ala Gly Trp Ile Gln Ala Gln Gln Leu Gln	
	245 250 255	
35	GGA GAC GCG CTG CGC CAG ATG CAG GTG CTG TAC GGC CAG CAC TTC CCC	816
	Gly Asp Ala Leu Arg Gln Met Gln Val Leu Tyr Gly Gln His Phe Pro	
	260 265 270	
40	ATC GAG GTC CGG CAC TAC TTG GCC CAG TGG ATT GAG AGC CAG CCA TGG	864
	Ile Glu Val Arg His Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp	
	275 280 285	
45	GAT GCC ATT GAC TTG GAC AAT CCC CAG GAC AGA GCC CAA GCC ACC CAG	912
	Asp Ala Ile Asp Leu Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln	
	290 295 300	
50	CTC CTG GAG GGC CTG GTG CAG GAG CTG CAG AAG AAG GCG GAG CAC CAG	960
	Leu Leu Glu Gly Leu Val Gln Glu Leu Gln Lys Lys Ala Glu His Gln	
	305 310 315 320	
55	GTG GGG GAA GAT GGG TTT TTA CTG AAG ATC AAG CTG GGG CAC TAC GCC	1008
	Val Gly Glu Asp Gly Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala	
	325 330 335	
60	ACG CAG CTC CAG AAA ACA TAT GAC CGC TGC CCC CTG GAG CTG GTC CGC	1056
	Thr Gln Leu Gln Lys Thr Tyr Asp Arg Cys Pro Leu Glu Leu Val Arg	
	340 345 350	
65	TGC ATC CGG CAC ATT CTG TAC AAT GAA CAG AGG CTG GTC CGA GAA GCC	1104
	Cys Ile Arg His Ile Leu Tyr Asn Glu Gln Arg Leu Val Arg Glu Ala	
	355 360 365	

111

112

	AAC AAT TGC AGC TCT CCG GCT GGG ATC CTG GTT GAC GCC ATG TCC CAG	1152
	Asn Asn Cys Ser Ser Pro Ala Gly Ile Leu Val Asp Ala Met Ser Gln	
	370 375 380	
5	AAG CAC CTT CAG ATC AAC CAG ACA TTT GAG GAG CTG CGA CTG GTC ACG	1200
	Lys His Leu Gln Ile Asn Gln Thr Phe Glu Glu Leu Arg Leu Val Thr	
	385 390 395 400	
10	CAG GAC ACA GAG AAT GAG CTG AAG AAA CTG CAG CAG ACT CAG GAG TAC	1248
	Gln Asp Thr Glu Asn Glu Leu Lys Lys Leu Gln Gln Thr Gln Glu Tyr	
	405 410 415	
15	TTC ATC ATC CAG TAC CAG GAG AGC CTG AGG ATC CAA GCT CAG TTT GCC	1296
	Phe Ile Ile Gln Tyr Gln Glu Ser Leu Arg Ile Gln Ala Gln Phe Ala	
	420 425 430	
20	CAG CTG GCC CAG CTG AGC CCC CAG GAG CGT CTG AGC CGG GAG ACG GCC	1344
	Gln Leu Ala Gln Leu Ser Pro Gln Glu Arg Leu Ser Arg Glu Thr Ala	
	435 440 445	
25	CTC CAG CAG AAG CAG GTG TCT CTG GAG GCC TGG TTG CAG CGT GAG GCA	1392
	Leu Gln Gln Lys Gln Val Ser Leu Glu Ala Trp Leu Gln Arg Glu Ala	
	450 455 460	
30	CAG ACA CTG CAG CAG TAC CGC GTG GAG CTG GCC GAG AAG CAC CAG AAG	1440
	Gln Thr Leu Gln Gln Tyr Arg Val Glu Leu Ala Glu Lys His Gln Lys	
	465 470 475 480	
35	ACC CTG CAG CTG CTG CGG AAG CAG CAG ACC ATC ATC CTG GAT GAC GAG	1488
	Thr Leu Gln Leu Leu Arg Lys Gln Gln Thr Ile Ile Leu Asp Asp Glu	
	485 490 495	
40	CTG ATC CAG TGG AAG CGG CGG CAG CAG CTG GCC GGG AAC GGC GGC CCC	1536
	Leu Ile Gln Trp Lys Arg Arg Gln Gln Leu Ala Gly Asn Gly Gly Pro	
	500 505 510	
45	CCC GAG GGC AGC CTG GAC GTG CTA CAG TCC TGG TGT GAG AAG TTG GCC	1584
	Pro Glu Gly Ser Leu Asp Val Leu Gln Ser Trp Cys Glu Lys Leu Ala	
	515 520 525	
50	GAG ATC ATC TGG CAG AAC CGG CAG CAG ATC CGC AGG GCT GAG CAC CTC	1632
	Glu Ile Ile Trp Gln Asn Arg Gln Gln Ile Arg Arg Ala Glu His Leu	
	530 535 540	
55	TGC CAG CAG CTG CCC ATC CCC GGC CCA GTG GAG GAG ATG CTG GCC GAG	1680
	Cys Gln Gln Leu Pro Ile Pro Gly Pro Val Glu Glu Met Leu Ala Glu	
	545 550 555 560	
60	GTC AAC GCC ACC ATC ACG GAC ATT ATC TCA GCC CTG GTG ACC AGC ACA	1728
	Val Asn Ala Thr Ile Thr Asp Ile Ile Ser Ala Leu Val Thr Ser Thr	
	565 570 575	
65	TTC ATC ATT GAG AAG CAG CCT CCT CAG GTC CTG AAG ACC CAG ACC AAG	1776
	Phe Ile Ile Glu Lys Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys	
	580 585 590	

112

113

	TTT GCA GCC ACC GTA CGC CTG CTG GTG GGC GGG AAG CTG AAC GTG CAC	1824
	Phe Ala Ala Thr Val Arg Leu Leu Val Gly Gly Lys Leu Asn Val His	
	595 600 605	
5	ATG AAT CCC CCC CAG GTG AAG GCC ACC ATC ATC AGT GAG CAG CAG GCC	1872
	Met Asn Pro Pro Gln Val Lys Ala Thr Ile Ile Ser Glu Gln Gln Ala	
	610 615 620	
10	AAG TCT CTG CTT AAA AAT GAG AAC ACC CGC AAC GAG TGC AGT GGT GAG	1920
	Lys Ser Leu Leu Lys Asn Glu Asn Thr Arg Asn Glu Cys Ser Gly Glu	
	625 630 635 640	
15	ATC CTG AAC AAC TGC TGC GTG ATG GAG TAC CAC CAA GCC ACG GGC ACC	1968
	Ile Leu Asn Asn Cys Cys Val Met Glu Tyr His Gln Ala Thr Gly Thr	
	645 650 655	
20	CTC AGT GCC CAC TTC AGG AAC ATG TCA CTG AAG AGG ATC AAG CGT GCT	2016
	Leu Ser Ala His Phe Arg Asn Met Ser Leu Lys Arg Ile Lys Arg Ala	
	660 665 670	
25	GAC CGG CGG GGT GCA GAG TCC GTG ACA GAG GAG AAG TTC ACA GTC CTG	2064
	Asp Arg Arg Gly Ala Glu Ser Val Thr Glu Glu Lys Phe Thr Val Leu	
	675 680 685	
30	TTT GAG TCT CAG TTC AGT GTT GGC AGC AAT GAG CTT GTG TTC CAG GTG	2112
	Phe Glu Ser Gln Phe Ser Val Gly Ser Asn Glu Leu Val Phe Gln Val	
	690 695 700	
35	AAG ACT CTG TCC CTA CCT GTG GTT GTC ATC GTC CAC GGC AGC CAG GAC	2160
	Lys Thr Leu Ser Leu Pro Val Val Val Ile Val His Gly Ser Gln Asp	
	705 710 715 720	
40	CAC AAT GCC ACG GCT ACT GTG CTG TGG GAC AAT GCC TTT GCT GAG CCG	2208
	His Asn Ala Thr Ala Thr Val Leu Trp Asp Asn Ala Phe Ala Glu Pro	
	725 730 735	
45	GGC AGG GTG CCA TTT GCC GTG CCT GAC AAA GTG CTG TGG CCG CAG CTG	2256
	Gly Arg Val Pro Phe Ala Val Pro Asp Lys Val Leu Trp Pro Gln Leu	
	740 745 750	
50	TGT GAG GCG CTC AAC ATG AAA TTC AAG GCC GAA GTG CAG AGC AAC CGG	2304
	Cys Glu Ala Leu Asn Met Lys Phe Lys Ala Glu Val Gln Ser Asn Arg	
	755 760 765	
55	GGC CTG ACC AAG GAG AAC CTC GTG TTC CTG GCG CAG AAA CTG TTC AAC	2352
	Gly Leu Thr Lys Glu Asn Leu Val Phe Leu Ala Gln Lys Leu Phe Asn	
	770 775 780	
60	AAC AGC AGC AGC CAC CTG GAG GAC TAC AGT GGC CTG TCC GTG TCC TGG	2400
	Asn Ser Ser Ser His Leu Glu Asp Tyr Ser Gly Leu Ser Val Ser Trp	
	785 790 795 800	
65	TCC CAG TTC AAC AGG GAG AAC TTG CCG GGC TGG AAC TAC ACC TTC TGG	2448
	Ser Gln Phe Asn Arg Glu Asn Leu Pro Gly Trp Asn Tyr Thr Phe Trp	
	805 810 815	

113

114

	CAG TGG TTT GAC GGG GTG ATG GAG GTG TTG AAG AAG CAC CAC AAG CCC Gln Trp Phe Asp Gly Val Met Glu Val Leu Lys Lys His His Lys Pro 820 825 830	2496
5	CAC TGG AAT GAT GGG GCC ATC CTA GGT TTT GTG AAT AAG CAA CAG GCC His Trp Asn Asp Gly Ala Ile Leu Gly Phe Val Asn Lys Gln Gln Ala 835 840 845	2544
10	CAC GAC CTG CTC ATC AAC AAG CCC GAC GGG ACC TTC TTG TTG CGC TTT His Asp Leu Leu Ile Asn Lys Pro Asp Gly Thr Phe Leu Leu Arg Phe 850 855 860	2592
15	AGT GAC TCA GAA ATC GGG GGC ATC ACC ATC GCC TGG AAG TTT GAC TCC Ser Asp Ser Glu Ile Gly Gly Ile Thr Ile Ala Trp Lys Phe Asp Ser 865 870 875 880	2640
20	CCG GAA CGC AAC CTG TGG AAC CTG AAA CCA TTC ACC ACG CGG GAT TTC Pro Glu Arg Asn Leu Trp Asn Leu Lys Pro Phe Thr Thr Arg Asp Phe 885 890 895	2688
	TCC ATC AGG TCC CTG GCT GAC CGG CTG GGG GAC CTG AGC TAT CTC ATC Ser Ile Arg Ser Leu Ala Asp Arg Leu Gly Asp Leu Ser Tyr Leu Ile 900 905 910	2736
25	TAT GTG TTT CCT GAC CGC CCC AAG GAT GAG GTC TTC TCC AAG TAC TAC Tyr Val Phe Pro Asp Arg Pro Lys Asp Glu Val Phe Ser Lys Tyr Tyr 915 920 925	2784
30	ACT CCT GTG CTG GCT AAA GCT GTT GAT GGA TAT GTG AAA CCA CAG ATC Thr Pro Val Leu Ala Lys Ala Val Asp Gly Tyr Val Lys Pro Gln Ile 930 935 940	2832
35	AAG CAA GTG GTC CCT GAG TTT GTG AAT GCA TCT GCA GAT GCT GGG GGC Lys Gln Val Val Pro Glu Phe Val Asn Ala Ser Ala Asp Ala Gly Gly 945 950 955 960	2880
40	AGC AGC GCC ACG TAC ATG GAC CAG GCC CCC TCC CCA GCT GTG TGC CCC Ser Ser Ala Thr Tyr Met Asp Gln Ala Pro Ser Pro Ala Val Cys Pro 965 970 975	2928
	CAG GCT CCC TAT AAC ATG TAC CCA CAG AAC CCT GAC CAT GTA CTC GAT Gln Ala Pro Tyr Asn Met Tyr Pro Gln Asn Pro Asp His Val Leu Asp 980 985 990	2976
45	CAG GAT GGA GAA TTC GAC CTG GAT GAG ACC ATG GAT GTG GCC AGG CAC Gln Asp Gly Glu Phe Asp Leu Asp Glu Thr Met Asp Val Ala Arg His 995 1000 1005	3024
50	GTG GAG GAA CTC TTA CGC CGA CCA ATG GAC AGT CTT GAC TCC CGC CTC Val Glu Glu Leu Leu Arg Arg Pro Met Asp Ser Leu Asp Ser Arg Leu 1010 1015 1020	3072
55	TCG CCC CCT GCC GGT CTT TTC ACC TCT GCC AGA GGC TCC CTC TCA TGA Ser Pro Pro Ala Gly Leu Phe Thr Ser Ala Arg Gly Ser Leu Ser 1025 1030 1035 1	3120

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1039 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```

15 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
    1           5           10           15
    Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
        20           25           30
20 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
    35           40           45
    Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50           55           60
    Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
    65           70           75           80
25 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
    85           90           95
    Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
    100          105          110
    Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
    115          120          125
30 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130          135          140
    Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
    145          150          155          160
35 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
    165          170          175
    Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
    180          185          190
    Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
    195          200          205
40 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    210          215          220
    Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
    225          230          235          240
45 Gly Leu Arg Ser Thr Met Ala Gly Trp Ile Gln Ala Gln Gln Leu Gln
    245          250          255
    Gly Asp Ala Leu Arg Gln Met Gln Val Leu Tyr Gly Gln His Phe Pro
    260          265          270
    Ile Glu Val Arg His Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp
    275          280          285
50 Asp Ala Ile Asp Leu Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln
    290          295          300
    Leu Leu Glu Gly Leu Val Gln Glu Leu Gln Lys Lys Ala Glu His Gln
    305          310          315          320
55 Val Gly Glu Asp Gly Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala
    325          330          335

```

116

Thr Gln Leu Gln Lys Thr Tyr Asp Arg Cys Pro Leu Glu Leu Val Arg  
 340 345 350  
 Cys Ile Arg His Ile Leu Tyr Asn Glu Gln Arg Leu Val Arg Glu Ala  
 355 360 365  
 5 Asn Asn Cys Ser Ser Pro Ala Gly Ile Leu Val Asp Ala Met Ser Gln  
 370 375 380  
 Lys His Leu Gln Ile Asn Gln Thr Phe Glu Glu Leu Arg Leu Val Thr  
 385 390 395 400  
 10 Gln Asp Thr Glu Asn Glu Leu Lys Lys Leu Gln Gln Thr Gln Glu Tyr  
 405 410 415  
 Phe Ile Ile Gln Tyr Gln Glu Ser Leu Arg Ile Gln Ala Gln Phe Ala  
 420 425 430  
 Gln Leu Ala Gln Leu Ser Pro Gln Glu Arg Leu Ser Arg Glu Thr Ala  
 435 440 445  
 15 Leu Gln Gln Lys Gln Val Ser Leu Glu Ala Trp Leu Gln Arg Glu Ala  
 450 455 460  
 Gln Thr Leu Gln Gln Tyr Arg Val Glu Leu Ala Glu Lys His Gln Lys  
 465 470 475 480  
 20 Thr Leu Gln Leu Leu Arg Lys Gln Gln Thr Ile Ile Leu Asp Asp Glu  
 485 490 495  
 Leu Ile Gln Trp Lys Arg Arg Gln Gln Leu Ala Gly Asn Gly Gly Pro  
 500 505 510  
 Pro Glu Gly Ser Leu Asp Val Leu Gln Ser Trp Cys Glu Lys Leu Ala  
 515 520 525  
 25 Glu Ile Ile Trp Gln Asn Arg Gln Gln Ile Arg Arg Ala Glu His Leu  
 530 535 540  
 Cys Gln Gln Leu Pro Ile Pro Gly Pro Val Glu Glu Met Leu Ala Glu  
 545 550 555 560  
 30 Val Asn Ala Thr Ile Thr Asp Ile Ile Ser Ala Leu Val Thr Ser Thr  
 565 570 575  
 Phe Ile Ile Glu Lys Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys  
 580 585 590  
 Phe Ala Ala Thr Val Arg Leu Leu Val Gly Gly Lys Leu Asn Val His  
 595 600 605  
 35 Met Asn Pro Pro Gln Val Lys Ala Thr Ile Ile Ser Glu Gln Gln Ala  
 610 615 620  
 Lys Ser Leu Leu Lys Asn Glu Asn Thr Arg Asn Glu Cys Ser Gly Glu  
 625 630 635 640  
 40 Ile Leu Asn Asn Cys Cys Val Met Glu Tyr His Gln Ala Thr Gly Thr  
 645 650 655  
 Leu Ser Ala His Phe Arg Asn Met Ser Leu Lys Arg Ile Lys Arg Ala  
 660 665 670  
 Asp Arg Arg Gly Ala Glu Ser Val Thr Glu Glu Lys Phe Thr Val Leu  
 675 680 685  
 45 Phe Glu Ser Gln Phe Ser Val Gly Ser Asn Glu Leu Val Phe Gln Val  
 690 695 700  
 Lys Thr Leu Ser Leu Pro Val Val Val Ile Val His Gly Ser Gln Asp  
 705 710 715 720  
 50 His Asn Ala Thr Ala Thr Val Leu Trp Asp Asn Ala Phe Ala Glu Pro  
 725 730 735  
 Gly Arg Val Pro Phe Ala Val Pro Asp Lys Val Leu Trp Pro Gln Leu  
 740 745 750  
 Cys Glu Ala Leu Asn Met Lys Phe Lys Ala Glu Val Gln Ser Asn Arg  
 755 760 765  
 55 Gly Leu Thr Lys Glu Asn Leu Val Phe Leu Ala Gln Lys Leu Phe Asn  
 770 775 780

116



117

Asn Ser Ser Ser His Leu Glu Asp Tyr Ser Gly Leu Ser Val Ser Trp  
 785 790 795 800  
 Ser Gln Phe Asn Arg Glu Asn Leu Pro Gly Trp Asn Tyr Thr Phe Trp  
 805 810 815  
 5 Gln Trp Phe Asp Gly Val Met Glu Val Leu Lys Lys His His Lys Pro  
 820 825 830  
 His Trp Asn Asp Gly Ala Ile Leu Gly Phe Val Asn Lys Gln Gln Ala  
 835 840 845  
 10 His Asp Leu Leu Ile Asn Lys Pro Asp Gly Thr Phe Leu Leu Arg Phe  
 850 855 860  
 Ser Asp Ser Glu Ile Gly Gly Ile Thr Ile Ala Trp Lys Phe Asp Ser  
 865 870 875 880  
 Pro Glu Arg Asn Leu Trp Asn Leu Lys Pro Phe Thr Thr Arg Asp Phe  
 885 890 895  
 15 Ser Ile Arg Ser Leu Ala Asp Arg Leu Gly Asp Leu Ser Tyr Leu Ile  
 900 905 910  
 Tyr Val Phe Pro Asp Arg Pro Lys Asp Glu Val Phe Ser Lys Tyr Tyr  
 915 920 925  
 20 Thr Pro Val Leu Ala Lys Ala Val Asp Gly Tyr Val Lys Pro Gln Ile  
 930 935 940  
 Lys Gln Val Val Pro Glu Phe Val Asn Ala Ser Ala Asp Ala Gly Gly  
 945 950 955 960  
 Ser Ser Ala Thr Tyr Met Asp Gln Ala Pro Ser Pro Ala Val Cys Pro  
 965 970 975  
 25 Gln Ala Pro Tyr Asn Met Tyr Pro Gln Asn Pro Asp His Val Leu Asp  
 980 985 990  
 Gln Asp Gly Glu Phe Asp Leu Asp Glu Thr Met Asp Val Ala Arg His  
 995 1000 1005  
 Val Glu Glu Leu Leu Arg Arg Pro Met Asp Ser Leu Asp Ser Arg Leu  
 1010 1015 1020  
 30 Ser Pro Pro Ala Gly Leu Phe Thr Ser Ala Arg Gly Ser Leu Ser  
 1025 1030 1035 1

(2) INFORMATION FOR SEQ ID NO:56:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1875 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

40

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

45

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1872

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

50

ATG GCG GCG GCG GCG GCG GCT CCG GGG GGC GGG GGC GGG GAG CCC AGG  
 Met Ala Ala Ala Ala Ala Ala Pro Gly Gly Gly Gly Gly Glu Pro Arg  
 1 5 10 15

48

55

GGA ACT GCT GGG GTC GTC CCG GTG GTC CCC GGG GAG GTG GAG GTG GTG  
 Gly Thr Ala Gly Val Val Pro Val Val Pro Gly Glu Val Glu Val Val

96

117

118															
	20				25				30						
5	AAG GGG CAG CCA TTC GAT GTG GGC CCA CGC TAC ACG CAG CTG CAG TAC	144													
	Lys Gly Gln Pro Phe Asp Val Gly Pro Arg Tyr Thr Gln Leu Gln Tyr														
	35 40 45														
10	ATC GGC GAG GGC GCG TAC GGC ATG GTC AGC TCA GCT TAT GAC CAC GTG	192													
	Ile Gly Glu Gly Ala Tyr Gly Met Val Ser Ser Ala Tyr Asp His Val														
	50 55 60														
15	CGC AAG ACC AGA GTG GCC ATC AAG AAG ATC AGC CCC TTT GAG CAT CAA	240													
	Arg Lys Thr Arg Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln														
	65 70 75 80														
20	ACC TAC TGT CAG CGC ACG CTG AGG GAG ATC CAG ATC TTG CTG CGA TTC	288													
	Thr Tyr Cys Gln Arg Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe														
	85 90 95														
25	CGC CAT GAG AAT GTT ATA GGC ATC CGA GAC ATC CTC AGA GCG CCC ACC	336													
	Arg His Glu Asn Val Ile Gly Ile Arg Asp Ile Leu Arg Ala Pro Thr														
	100 105 110														
30	CTG GAA GCC ATG AGA GAT GTT TAC ATT GTT CAG GAC CTC ATG GAG ACA	384													
	Leu Glu Ala Met Arg Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr														
	115 120 125														
35	GAC CTG TAC AAG CTG CTT AAA AGC CAG CAG CTG AGC AAT GAC CAC ATC	432													
	Asp Leu Tyr Lys Leu Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile														
	130 135 140														
40	TGC TAC TTC CTC TAC CAG ATC CTC CGG GGC CTC AAG TAT ATA CAC TCA	480													
	Cys Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser														
	145 150 155 160														
45	GCC AAT GTG CTG CAC CGG GAC CTG AAG CCT TCC AAT CTG CTT ATC AAC	528													
	Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Ile Asn														
	165 170 175														
50	ACC ACC TGC GAC CTT AAG ATC TGT GAT TTT GGC CTG GCC CGG ATT GCT	576													
	Thr Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala														
	180 185 190														
55	GAC CCT GAG CAC GAC CAC ACT GGC TTT CTG ACG GAG TAT GTG GCC ACA	624													
	Asp Pro Glu His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr														
	195 200 205														
60	CGC TGG TAC CGA GCC CCA GAG ATC ATG CTT AAT TCC AAG GGC TAC ACC	672													
	Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr														
	210 215 220														
65	AAA TCC ATC GAC ATC TGG TCT GTG GGC TGC ATT CTG GCT GAG ATG CTC	720													
	Lys Ser Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu														
	225 230 235 240														
70	TCC AAC CGG CCC ATC TTC CCC GGC AAG CAC TAC CTG GAC CAG CTC AAC	768													
	Ser Asn Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn														

	245	250	255	
5	CAC ATT CTA GGT ATC TTG GGT TCC CCA His Ile Leu Gly Ile Leu Gly Ser Pro	TCC CAG GAG GAC CTT AAT TGC Ser Gln Glu Asp Leu Asn Cys	816	
	260	265	270	
10	ATC ATT AAC ATG AAG GCC CGA AAC TAC CTG CAG TCT CTG CCC TCG AAA Ile Ile Asn Met Lys Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys	864		
	275	280	285	
15	ACC AAG GTG GCT TGG GCC AAG CTC TTT CCT AAA TCT GAC TCC AAA GCT Thr Lys Val Ala Trp Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala	912		
	290	295	300	
20	CTT GAC CTG CTG GAC CGG ATG TTA ACC TTC AAC CCA AAC AAG CGC ATC Leu Asp Leu Leu Asp Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile	960		
	305	310	315	320
25	ACA GTA GAG GAA GCG CTG GCT CAC CCT TAC CTG GAA CAG TAC TAC GAT Thr Val Glu Glu Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp	1008		
	325	330	335	
30	CCG ACA GAT GAG CCA GTG GCC GAG GAG CCA TTC ACC TTC GAC ATG GAG Pro Thr Asp Glu Pro Val Ala Glu Glu Pro Phe Thr Phe Asp Met Glu	1056		
	340	345	350	
35	CTG GAT GAC CTC CCC AAG GAG CGG CTG AAG GAG TTG ATC TTC CAG GAG Leu Asp Asp Leu Pro Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu	1104		
	355	360	365	
40	ACA GCC CGC TTC CAG CCA GGG GCG CCA GAG GGC CCC GGG CGC GCC ATG Thr Ala Arg Phe Gln Pro Gly Ala Pro Glu Gly Pro Gly Arg Ala Met	1152		
	370	375	380	
45	AGT AAA GGA GAA GAA CTT TTC ACT GGA GTT GTC CCA ATT CTT GTT GAA Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu	1200		
	385	390	395	400
50	TTA GAT GGC GAT GTT AAT GGG CAA AAA TTC TCT GTT AGT GGA GAG GGT Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu Gly	1248		
	405	410	415	
55	GAA GGT GAT GCA ACA TAC GGA AAA CTT ACC CTT AAA TTT ATT TGC ACT Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr	1296		
	420	425	430	
60	ACT GGG AAG CTA CCT GTT CCA TGG CCA ACG CTT GTC ACT ACT CTC ACT Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr	1344		
	435	440	445	
65	TAT GGT GTT CAA TGC TTT TCT AGA TAC CCA GAT CAT ATG AAA CAG CAT Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His	1392		
	450	455	460	
70	GAC TTT TTC AAG AGT GCC ATG CCC GAA GGT TAT GTA CAG GAA AGA ACT Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr	1440		

[illegible]

(2) INFORMATION FOR SEO ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 624 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEO ID NO:57:

55 Met Ala Ala Ala Ala Ala Ala Pro Gly Gly Gly Gly Gly Glu Pro Arg  
1 5 10 15  
Gly Thr Ala Gly Val Val Pro Val Val Pro Gly Glu Val Glu Val Val

121

20 25 30  
 Lys Gly Gln Pro Phe Asp Val Gly Pro Arg Tyr Thr Gln Leu Gln Tyr  
 35 40 45  
 5 Ile Gly Glu Gly Ala Tyr Gly Met Val Ser Ser Ala Tyr Asp His Val  
 50 55 60  
 Arg Lys Thr Arg Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln  
 65 70 75 80  
 Thr Tyr Cys Gln Arg Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe  
 85 90 95  
 10 Arg His Glu Asn Val Ile Gly Ile Arg Asp Ile Leu Arg Ala Pro Thr  
 100 105 110  
 Leu Glu Ala Met Arg Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr  
 115 120 125  
 15 Asp Leu Tyr Lys Leu Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile  
 130 135 140  
 Cys Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser  
 145 150 155 160  
 Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Ile Asn  
 165 170 175  
 20 Thr Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala  
 180 185 190  
 Asp Pro Glu His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr  
 195 200 205  
 25 Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr  
 210 215 220  
 Lys Ser Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu  
 225 230 235 240  
 Ser Asn Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn  
 245 250 255  
 30 His Ile Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys  
 260 265 270  
 Ile Ile Asn Met Lys Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys  
 275 280 285  
 35 Thr Lys Val Ala Trp Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala  
 290 295 300  
 Leu Asp Leu Leu Asp Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile  
 305 310 315 320  
 Thr Val Glu Glu Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp  
 325 330 335  
 40 Pro Thr Asp Glu Pro Val Ala Glu Glu Pro Phe Thr Phe Asp Met Glu  
 340 345 350  
 Leu Asp Asp Leu Pro Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu  
 355 360 365  
 45 Thr Ala Arg Phe Gln Pro Gly Ala Pro Glu Gly Pro Gly Arg Ala Met  
 370 375 380  
 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu  
 385 390 395 400  
 Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu Gly  
 405 410 415  
 50 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr  
 420 425 430  
 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr  
 435 440 445  
 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His  
 450 455 460  
 55 Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr

121

122

465                      470                      475                      480  
 Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys  
                                  485                      490                      495  
 5 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp  
                                  500                      505                      510  
 Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn Tyr  
                                  515                      520                      525  
 Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly Ile  
                                  530                      535                      540  
 10 Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val Gln  
                                  545                      550                      555                      560  
 Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val  
                                  565                      570                      575  
 15 Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys  
                                  580                      585                      590  
 Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val Thr  
                                  595                      600                      605  
 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro Gln Glu  
                                  610                      615                      620  
 20

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 1815 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

30

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...1811  
 (D) OTHER INFORMATION:

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

40      1                      5                      10                      15                      48  
 ATG GCG GCG GCG GCG GCG GCG GGC CCG GAG ATG GTC CGC GGG CAG GTG  
 Met Ala Ala Ala Ala Ala Gly Pro Glu Met Val Arg Gly Gln Val  
 45      20                      25                      30                      96  
 TTC GAC GTG GGG CCG CGC TAC ACT AAT CTC TCG TAC ATC GGA GAA GGC  
 Phe Asp Val Gly Pro Arg Tyr Thr Asn Leu Ser Tyr Ile Gly Glu Gly  
 50      35                      40                      45                      144  
 GCC TAC GGC ATG GTT TGT TCT GCT TAT GAT AAT CTC AAC AAA GTT CGA  
 Ala Tyr Gly Met Val Cys Ser Ala Tyr Asp Asn Leu Asn Lys Val Arg  
 55      50                      55                      60                      192  
 GTT GCT ATC AAG AAA ATC AGT CCT TTT GAG CAC CAG ACC TAC TGT CAG  
 Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln  
 65                      70                      75                      80                      240  
 AGA ACC CTG AGA GAG ATA AAA ATC CTA CTG CGC TTC AGA CAT GAG AAC  
 Arg Thr Leu Arg Glu Ile Lys Ile Leu Leu Arg Phe Arg His Glu Asn

122

123

5	ATC ATC GGC ATC AAT GAC ATC ATC CGG GCA CCA ACC ATT GAG CAG ATG Ile Ile Gly Ile Asn Asp Ile Ile Arg Ala Pro Thr Ile Glu Gln Met 85 90 95	288
	AAA GAT GTA TAT ATA GTA CAG GAC CTC ATG GAG ACA GAT CTT TAC AAG Lys Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys 100 105 110	336
	CTC TTG AAG ACA CAG CAC CTC AGC AAT GAT CAT ATC TGC TAT TTT CTT Leu Leu Lys Thr Gln His Leu Ser Asn Asp His Ile Cys Tyr Phe Leu 115 120 125	384
	TAT CAG ATC CTG AGA GGA TTA AAG TAT ATA CAT TCA GCT AAT GTT CTG Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu 130 135 140	432
	CAC CGT GAC CTC AAG CCT TCC AAC CTC CTG CTG AAC ACC ACT TGT GAT His Arg Asp Leu Lys Pro Ser Asn Leu Leu Asn Thr Thr Cys Asp 145 150 155 160	480
20	CTC AAG ATC TGT GAC TTT GGC CTT GCC CGT GTT GCA GAT CCA GAC CAT Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Val Ala Asp Pro Asp His 165 170 175	528
	GAT CAT ACA GGG TTC TTG ACA GAG TAT GTA GCC ACG CGT TGG TAC AGA Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg 180 185 190	576
	GCT CCA GAA ATT ATG TTG AAT TCC AAG GGT TAT ACC AAG TCC ATT GAT Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile Asp 195 200 205	624
	ATT TGG TCT GTG GGC TGC ATC CTG GCA GAG ATG CTA TCC AAC AGG CCT Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg Pro 210 215 220	672
	ATC TTC CCA GGA AAG CAT TAC CTT GAC CAG CTG AAT CAC ATC CTG GGT Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu Gly 225 230 235 240	720
40	ATT CTT GGA TCT CCA TCA CAG GAA GAT CTG AAT TGT ATA ATA AAT TTA Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn Leu 245 250 255	768
	AAA GCT AGA AAC TAT TTG CTT TCT CTC CCG CAC AAA AAT AAG GTG CCG Lys Ala Arg Asn Tyr Leu Leu Ser Leu Pro His Lys Asn Lys Val Pro 260 265 270	816
	TGG AAC AGG TTG TTC CCA AAC GCT GAC TCC AAA GCT CTG GAT TTA CTG Trp Asn Arg Leu Phe Pro Asn Ala Asp Ser Lys Ala Leu Asp Leu Leu 275 280 285	864
	GAT AAA ATG TTG ACA TTT AAC CCT CAC AAG AGG ATT GAA GTT GAA CAG Asp Lys Met Leu Thr Phe Asn Pro His Lys Arg Ile Glu Val Glu Gln 290 295 300	912

123

124

5	GCT CTG GCC CAC CCG TAC CTG GAG CAG TAT TAT GAC CCA AGT GAT GAG Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Ser Asp Glu 305 310 315 320	960
10	CCC ATT GCT GAA GCA CCA TTC AAG TTT GAC ATG GAG CTG GAC GAC TTA Pro Ile Ala Glu Ala Pro Phe Lys Phe Asp Met Glu Leu Asp Asp Leu 325 330 335	1008
15	CCT AAG GAG AAG CTC AAA GAA CTC ATT TTT GAA GAG ACT GCT CGA TTC Pro Lys Glu Lys Leu Lys Glu Leu Ile Phe Glu Glu Thr Ala Arg Phe 340 345 350	1056
20	CAG CCA GGA TAC AGA TCT ATG GAT CCA CCG GTC GCC ACC ATG GTG AGC Gln Pro Gly Tyr Arg Ser Met Asp Pro Pro Val Ala Thr Met Val Ser 355 360 365	1104
25	AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG GTC GAG CTG Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu 370 375 380	1152
30	GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG GGC GAG Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu 385 390 395 400	1200
35	GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC TGC ACC ACC Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr 405 410 415	1248
40	GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC CTG ACC TAC Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr 420 425 430	1296
45	GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG CAG CAC GAC Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp 435 440 445	1344
50	TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG CGC ACC ATC Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile 450 455 460	1392
55	TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG GTG AAG TTC Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe 465 470 475 480	1440
60	GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC ATC GAC TTC Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe 485 490 495	1488
65	AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC AAC TAC AAC Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn 500 505 510	1536
70	AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC GGC ATC AAG Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys 515 520 525	1584

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125

5 GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG CAG CTC 1632  
 Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu  
 530 535 540  
 GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG 1680  
 Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu  
 545 550 555 560  
 10 CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC 1728  
 Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp  
 565 570 575  
 15 CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC 1776  
 Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala  
 580 585 590  
 20 GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AA GTAA 1815  
 Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 595 600

## (2) INFORMATION FOR SEQ ID NO:59:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 604 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:  
 Met Ala Ala Ala Ala Ala Gly Pro Glu Met Val Arg Gly Gln Val  
 1 5 10 15  
 Phe Asp Val Gly Pro Arg Tyr Thr Asn Leu Ser Tyr Ile Gly Glu Gly  
 20 25 30  
 40 Ala Tyr Gly Met Val Cys Ser Ala Tyr Asp Asn Leu Asn Lys Val Arg  
 35 40 45  
 Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln  
 50 55 60  
 Arg Thr Leu Arg Glu Ile Lys Ile Leu Leu Arg Phe Arg His Glu Asn  
 45 65 70 75 80  
 Ile Ile Gly Ile Asn Asp Ile Ile Arg Ala Pro Thr Ile Glu Gln Met  
 85 90 95  
 Lys Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys  
 100 105 110  
 50 Leu Leu Lys Thr Gln His Leu Ser Asn Asp His Ile Cys Tyr Phe Leu  
 115 120 125  
 Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu  
 130 135 140  
 His Arg Asp Leu Lys Pro Ser Asn Leu Leu Leu Asn Thr Thr Cys Asp  
 55 145 150 155 160  
 Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Val Ala Asp Pro Asp His

125

	126										175									
	165					170					175									
	Asp	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg				
				180					185					190						
5	Ala	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys	Gly	Tyr	Thr	Lys	Ser	Ile	Asp				
			195					200					205							
	Ile	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala	Glu	Met	Leu	Ser	Asn	Arg	Pro				
		210					215					220								
	Ile	Phe	Pro	Gly	Lys	His	Tyr	Leu	Asp	Gln	Leu	Asn	His	Ile	Leu	Gly				
10	225					230					235					240				
	Ile	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp	Leu	Asn	Cys	Ile	Ile	Asn	Leu				
				245						250					255					
	Lys	Ala	Arg	Asn	Tyr	Leu	Leu	Ser	Leu	Pro	His	Lys	Asn	Lys	Val	Pro				
			260					265					270							
15	Trp	Asn	Arg	Leu	Phe	Pro	Asn	Ala	Asp	Ser	Lys	Ala	Leu	Asp	Leu	Leu				
		275					280					285								
	Asp	Lys	Met	Leu	Thr	Phe	Asn	Pro	His	Lys	Arg	Ile	Glu	Val	Glu	Gln				
	290					295					300									
	Ala	Leu	Ala	His	Pro	Tyr	Leu	Glu	Gln	Tyr	Tyr	Asp	Pro	Ser	Asp	Glu				
20	305					310					315					320				
	Pro	Ile	Ala	Glu	Ala	Pro	Phe	Lys	Phe	Asp	Met	Glu	Leu	Asp	Asp	Leu				
				325						330					335					
	Pro	Lys	Glu	Lys	Leu	Lys	Glu	Leu	Ile	Phe	Glu	Glu	Thr	Ala	Arg	Phe				
			340					345					350							
25	Gln	Pro	Gly	Tyr	Arg	Ser	Met	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser				
		355					360					365								
	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu				
	370					375					380									
	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu				
30	385					390					395					400				
	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr				
				405						410					415					
	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr				
			420					425					430							
35	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp				
		435					440					445								
	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile				
	450					455					460									
	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe				
40	465					470					475					480				
	Glu	Gly	Asp	Thr	Leu															

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## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2511 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## 10 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2508

(D) OTHER INFORMATION:

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

20	ATG GAG CTG GAA AAC ATC GTG GCC AAC ACG GTC TTG CTG AAA GCC AGG Met Glu Leu Glu Asn Ile Val Ala Asn Thr Val Leu Leu Lys Ala Arg	48
	1 5 10 15	
	GAA GGG GGC GGA GGA AAG CGC AAA GGG AAA AGC AAG AAG TGG AAA GAA Glu Gly Gly Gly Gly Lys Arg Lys Gly Lys Ser Lys Lys Trp Lys Glu	96
	20 25 30	
25	ATC CTG AAG TTC CCT CAC ATT AGC CAG TGT GAA GAC CTC CGA AGG ACC Ile Leu Lys Phe Pro His Ile Ser Gln Cys Glu Asp Leu Arg Arg Thr	144
	35 40 45	
30	ATA GAC AGA GAT TAC TGC AGT TTA TGT GAC AAG CAG CCA ATC GGG AGG Ile Asp Arg Asp Tyr Cys Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg	192
	50 55 60	
35	CTG CTT TTC CGG CAG TTT TGT GAA ACC AGG CCT GGG CTG GAG TGT TAC Leu Leu Phe Arg Gln Phe Cys Glu Thr Arg Pro Gly Leu Glu Cys Tyr	240
	65 70 75 80	
	ATT CAG TTC CTG GAC TCC GTG GCA GAA TAT GAA GTT ACT CCA GAT GAA Ile Gln Phe Leu Asp Ser Val Ala Glu Tyr Glu Val Thr Pro Asp Glu	288
40	85 90 95	
	AAA CTG GGA GAG AAA GGG AAG GAA ATT ATG ACC AAG TAC CTC ACC CCA Lys Leu Gly Glu Lys Gly Lys Glu Ile Met Thr Lys Tyr Leu Thr Pro	336
	100 105 110	
45	AAG TCC CCT GTT TTC ATA GCC CAA GTT GGC CAA GAC CTG GTC TCC CAG Lys Ser Pro Val Phe Ile Ala Gln Val Gly Gln Asp Leu Val Ser Gln	384
	115 120 125	
50	ACG GAG GAG AAG CTC CTA CAG AAG CCG TGC AAA GAA CTC TTT TCT GCC Thr Glu Glu Lys Leu Leu Gln Lys Pro Cys Lys Glu Leu Phe Ser Ala	432
	130 135 140	
55	TGT GCA CAG TCT GTC CAC GAG TAC CTG AGG GGA GAA CCA TTC CAC GAA Cys Ala Gln Ser Val His Glu Tyr Leu Arg Gly Glu Pro Phe His Glu	480
	145 150 155 160	

127

128

5	TAT CTG GAC AGC ATG TTT TTT GAC CGC TTT CTC CAG TGG AAG TGG TTG	528
	Tyr Leu Asp Ser Met Phe Phe Asp Arg Phe Leu Gln Trp Lys Trp Leu	
	165 170 175	
10	GAA AGG CAA CCG GTG ACC AAA AAC ACT TTC AGG CAG TAT CGA GTG CTA	576
	Glu Arg Gln Pro Val Thr Lys Asn Thr Phe Arg Gln Tyr Arg Val Leu	
	180 185 190	
15	GGA AAA GGG GGC TTC GGG GAG GTC TGT GCC TGC CAG GTT CGG GCC ACG	624
	Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala Thr	
	195 200 205	
20	GGT AAA ATG TAT GCC TGC AAG CGC TTG GAG AAG AAG AGG ATC AAA AAG	672
	Gly Lys Met Tyr Ala Cys Lys Arg Leu Glu Lys Lys Arg Ile Lys Lys	
	210 215 220	
25	AGG AAA GGG GAG TCC ATG GCC CTC AAT GAG AAG CAG ATC CTC GAG AAG	720
	Arg Lys Gly Glu Ser Met Ala Leu Asn Glu Lys Gln Ile Leu Glu Lys	
	225 230 235 240	
30	GTC AAC AGT CAG TTT GTG GTC AAC CTG GCC TAT GCC TAC GAG ACC AAG	768
	Val Asn Ser Gln Phe Val Val Asn Leu Ala Tyr Ala Tyr Glu Thr Lys	
	245 250 255	
35	GAT GCA CTG TGC TTG GTC CTG ACC ATC ATG AAT GGG GGT GAC CTG AAG	816
	Asp Ala Leu Cys Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu Lys	
	260 265 270	
40	TTC CAC ATC TAC AAC ATG GGC AAC CCT GGC TTC GAG GAG GAG CGG GCC	864
	Phe His Ile Tyr Asn Met Gly Asn Pro Gly Phe Glu Glu Glu Arg Ala	
	275 280 285	
45	TTG TTT TAT GCG GCA GAG ATC CTC TGC GGC TTA GAA GAC CTC CAC CGT	912
	Leu Phe Tyr Ala Ala Glu Ile Leu Cys Gly Leu Glu Asp Leu His Arg	
	290 295 300	
50	GAG AAC ACC GTC TAC CGA GAT CTG AAA CCT GAA AAC ATC CTG TTA GAT	960
	Glu Asn Thr Val Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp	
	305 310 315 320	
55	GAT TAT GGC CAC ATT AGG ATC TCA GAC CTG GGC TTG GCT GTG AAG ATC	1008
	Asp Tyr Gly His Ile Arg Ile Ser Asp Leu Gly Leu Ala Val Lys Ile	
	325 330 335	
60	CCC GAG GGA GAC CTG ATC CGC GGC CGG GTG GGC ACT GTT GGC TAC ATG	1056
	Pro Glu Gly Asp Leu Ile Arg Gly Arg Val Gly Thr Val Gly Tyr Met	
	340 345 350	
65	GCC CCC GAA GTC CTG AAC AAC CAG AGG TAC GGC CTG AGC CCC GAC TAC	1104
	Ala Pro Glu Val Leu Asn Asn Gln Arg Tyr Gly Leu Ser Pro Asp Tyr	
	355 360 365	
70	TGG GGC CTT GGC TGC CTC ATC TAT GAG ATG ATC GAG GGC CAG TCG CCG	1152
	Trp Gly Leu Gly Cys Leu Ile Tyr Glu Met Ile Glu Gly Gln Ser Pro	
	370 375 380	

128

129

5	TTC CGC GGC CGT AAG GAG AAG GTG AAG CGG GAG GAG GTG GAC CGC CGG Phe Arg Gly Arg Lys Glu Lys Val Lys Arg Glu Glu Val Asp Arg Arg 385 390 395 400	1200
10	GTC CTG GAG ACG GAG GAG GTG TAC TCC CAC AAG TTC TCC GAG GAG GCC Val Leu Glu Thr Glu Glu Val Tyr Ser His Lys Phe Ser Glu Glu Ala 405 410 415	1248
15	AAG TCC ATC TGC AAG ATG CTG CTC ACG AAA GAT GCG AAG CAG AGG CTG Lys Ser Ile Cys Lys Met Leu Leu Thr Lys Asp Ala Lys Gln Arg Leu 420 425 430	1296
20	GGC TGC CAG GAG GAG GGG GCT GCA GAG GTC AAG AGA CAC CCC TTC TTC Gly Cys Gln Glu Glu Gly Ala Ala Glu Val Lys Arg His Pro Phe Phe 435 440 445	1344
25	AGG AAC ATG AAC TTC AAG CGC TTA GAA GCC GGG ATG TTG GAC CCT CCC Arg Asn Met Asn Phe Lys Arg Leu Glu Ala Gly Met Leu Asp Pro Pro 450 455 460	1392
30	TTC GTT CCA GAC CCC CGC GCT GTG TAC TGT AAG GAC GTG CTG GAC ATC Phe Val Pro Asp Pro Arg Ala Val Tyr Cys Lys Asp Val Leu Asp Ile 465 470 475 480	1440
35	GAG CAG TTC TCC ACT GTG AAG GGC GTC AAT CTG GAC CAC ACA GAC GAC Glu Gln Phe Ser Thr Val Lys Gly Val Asn Leu Asp His Thr Asp Asp 485 490 495	1488
40	GAC TTC TAC TCC AAG TTC TCC ACG GGC TCT GTG TCC ATC CCA TGG CAA Asp Phe Tyr Ser Lys Phe Ser Thr Gly Ser Val Ser Ile Pro Trp Gln 500 505 510	1536
45	AAC GAG ATG ATA GAA ACA GAA TGC TTT AAG GAG CTG AAC GTG TTT GGA Asn Glu Met Ile Glu Thr Glu Cys Phe Lys Glu Leu Asn Val Phe Gly 515 520 525	1584
50	CCT AAT GGT ACC CTC CCG CCA GAT CTG AAC AGA AAC CAC CCT CCG GAA Pro Asn Gly Thr Leu Pro Pro Asp Leu Asn Arg Asn His Pro Pro Glu 530 535 540	1632
55	CCG CCC AAG AAA GGG CTG CTC CAG AGA CTC TTC AAG CGG CAG CAT CAG Pro Pro Lys Lys Gly Leu Leu Gln Arg Leu Phe Lys Arg Gln His Gln 545 550 555 560	1680
60	AAC AAT TCC AAG AGT TCG CCC AGC TCC AAG ACC AGT TTT AAC CAC CAC Asn Asn Ser Lys Ser Ser Pro Ser Ser Lys Thr Ser Phe Asn His His 565 570 575	1728
65	ATA AAC TCA AAC CAT GTC AGC TCG AAC TCC ACC GGA AGC AGC AGG GAT Ile Asn Ser Asn His Val Ser Ser Asn Ser Thr Gly Ser Ser Arg Asp 580 585 590	1776
70	CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly 595 600 605	1824

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130

5	GTG GTG CCC ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG	1872
	Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys	
	610 615 620	
10	TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG	1920
	Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu	
	625 630 635 640	
15	ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC	1968
	Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro	
	645 650 655	
20	ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC	2016
	Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr	
	660 665 670	
25	CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA	2064
	Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu	
	675 680 685	
30	GGC TAC GTC CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC	2112
	Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr	
	690 695 700	
35	AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC	2160
	Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg	
	705 710 715 720	
40	ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG	2208
	Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly	
	725 730 735	
45	CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC	2256
	His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala	
	740 745 750	
50	GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC	2304
	Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn	
	755 760 765	
55	ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC	2352
	Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr	
	770 775 780	
60	CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC	2400
	Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser	
	785 790 795 800	
65	ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG	2448
	Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met	
	805 810 815	
70	GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC	2496
	Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp	
	820 825 830	

130

GAG CTG TAC AAG TAA  
 Glu Leu Tyr Lys  
 835

2511

5

## (2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 836 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

20 Met Glu Leu Glu Asn Ile Val Ala Asn Thr Val Leu Leu Lys Ala Arg  
 1 5 10 15  
 Glu Gly Gly Gly Gly Lys Arg Lys Gly Lys Ser Lys Lys Trp Lys Glu  
 20 25 30  
 25 Ile Leu Lys Phe Pro His Ile Ser Gln Cys Glu Asp Leu Arg Arg Thr  
 35 40 45  
 Ile Asp Arg Asp Tyr Cys Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg  
 50 55 60  
 Leu Leu Phe Arg Gln Phe Cys Glu Thr Arg Pro Gly Leu Glu Cys Tyr  
 65 70 75 80  
 30 Ile Gln Phe Leu Asp Ser Val Ala Glu Tyr Glu Val Thr Pro Asp Glu  
 85 90 95  
 Lys Leu Gly Glu Lys Gly Lys Glu Ile Met Thr Lys Tyr Leu Thr Pro  
 100 105 110  
 Lys Ser Pro Val Phe Ile Ala Gln Val Gly Gln Asp Leu Val Ser Gln  
 115 120 125  
 35 Thr Glu Glu Lys Leu Leu Gln Lys Pro Cys Lys Glu Leu Phe Ser Ala  
 130 135 140  
 Cys Ala Gln Ser Val His Glu Tyr Leu Arg Gly Glu Pro Phe His Glu  
 145 150 155 160  
 40 Tyr Leu Asp Ser Met Phe Phe Asp Arg Phe Leu Gln Trp Lys Trp Leu  
 165 170 175  
 Glu Arg Gln Pro Val Thr Lys Asn Thr Phe Arg Gln Tyr Arg Val Leu  
 180 185 190  
 45 Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala Thr  
 195 200 205  
 Gly Lys Met Tyr Ala Cys Lys Arg Leu Glu Lys Lys Arg Ile Lys Lys  
 210 215 220  
 Arg Lys Gly Glu Ser Met Ala Leu Asn Glu Lys Gln Ile Leu Glu Lys  
 225 230 235 240  
 50 Val Asn Ser Gln Phe Val Val Asn Leu Ala Tyr Ala Tyr Glu Thr Lys  
 245 250 255  
 Asp Ala Leu Cys Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu Lys  
 260 265 270  
 55 Phe His Ile Tyr Asn Met Gly Asn Pro Gly Phe Glu Glu Arg Ala  
 275 280 285  
 Leu Phe Tyr Ala Ala Glu Ile Leu Cys Gly Leu Glu Asp Leu His Arg

131

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290                      295                      300  
 Glu Asn Thr Val Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp  
 305                      310                      315                      320  
 5 Asp Tyr Gly His Ile Arg Ile Ser Asp Leu Gly Leu Ala Val Lys Ile  
                     325                      330                      335  
 Pro Glu Gly Asp Leu Ile Arg Gly Arg Val Gly Thr Val Gly Tyr Met  
                     340                      345                      350  
 Ala Pro Glu Val Leu Asn Asn Gln Arg Tyr Gly Leu Ser Pro Asp Tyr  
                     355                      360                      365  
 10 Trp Gly Leu Gly Cys Leu Ile Tyr Glu Met Ile Glu Gly Gln Ser Pro  
                     370                      375                      380  
 Phe Arg Gly Arg Lys Glu Lys Val Lys Arg Glu Glu Val Asp Arg Arg  
 385                      390                      395                      400  
 15 Val Leu Glu Thr Glu Glu Val Tyr Ser His Lys Phe Ser Glu Glu Ala  
                     405                      410                      415  
 Lys Ser Ile Cys Lys Met Leu Leu Thr Lys Asp Ala Lys Gln Arg Leu  
                     420                      425                      430  
 Gly Cys Gln Glu Glu Gly Ala Ala Glu Val Lys Arg His Pro Phe Phe  
                     435                      440                      445  
 20 Arg Asn Met Asn Phe Lys Arg Leu Glu Ala Gly Met Leu Asp Pro Pro  
                     450                      455                      460  
 Phe Val Pro Asp Pro Arg Ala Val Tyr Cys Lys Asp Val Leu Asp Ile  
 465                      470                      475                      480  
 25 Glu Gln Phe Ser Thr Val Lys Gly Val Asn Leu Asp His Thr Asp Asp  
                     485                      490                      495  
 Asp Phe Tyr Ser Lys Phe Ser Thr Gly Ser Val Ser Ile Pro Trp Gln  
                     500                      505                      510  
 Asn Glu Met Ile Glu Thr Glu Cys Phe Lys Glu Leu Asn Val Phe Gly  
                     515                      520                      525  
 30 Pro Asn Gly Thr Leu Pro Pro Asp Leu Asn Arg Asn His Pro Pro Glu  
                     530                      535                      540  
 Pro Pro Lys Lys Gly Leu Leu Gln Arg Leu Phe Lys Arg Gln His Gln  
 545                      550                      555                      560  
 35 Asn Asn Ser Lys Ser Ser Pro Ser Ser Lys Thr Ser Phe Asn His His  
                     565                      570                      575  
 Ile Asn Ser Asn His Val Ser Ser Asn Ser Thr Gly Ser Ser Arg Asp  
                     580                      585                      590  
 Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly  
                     595                      600                      605  
 40 Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys  
                     610                      615                      620  
 Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu  
 625                      630                      635                      640  
 45 Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro  
                     645                      650                      655  
 Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr  
                     660                      665                      670  
 Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu  
                     675                      680                      685  
 50 Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr  
                     690                      695                      700  
 Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg  
 705                      710                      715                      720  
 55 Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly  
                     725                      730                      735  
 His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala

132



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740 745 750  
 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn  
 755 760 765  
 5 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr  
 770 775 780  
 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser  
 785 790 795 800  
 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met  
 805 810 815  
 10 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp  
 820 825 830  
 Glu Leu Tyr Lys  
 835

15 (2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1893 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

25 (A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1890

(D) OTHER INFORMATION:

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATG AGC AGA AGC AAG CGT GAC AAC AAT TTT TAT AGT GTA GAG ATT GGA 48  
 Met Ser Arg Ser Lys Arg Asp Asn Asn Phe Tyr Ser Val Glu Ile Gly  
 1 5 10 15  
 35 GAT TCT ACA TTC ACA GTC CTG AAA CGA TAT CAG AAT TTA AAA CCT ATA 96  
 Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro Ile  
 20 25 30  
 40 GGC TCA GGA GCT CAA GGA ATA GTA TGC GCA GCT TAT GAT GCC ATT CTT 144  
 Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Ile Leu  
 35 40 45  
 45 GAA AGA AAT GTT GCA ATC AAG AAG CTA AGC CGA CCA TTT CAG AAT CAG 192  
 Glu Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln  
 50 55 60  
 ACT CAT GCC AAG CGG GCC TAC AGA GAG CTA GTT CTT ATG AAA TGT GTT 240  
 Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys Val  
 50 65 70 75 80  
 AAT CAC AAA AAT ATA ATT GGC CTT TTG AAT GTT TTC ACA CCA CAG AAA 288  
 Asn His Lys Asn Ile Ile Gly Leu Leu Asn Val Phe Thr Pro Gln Lys  
 85 90 95  
 55 TCC CTA GAA GAA TTT CAA GAT GTT TAC ATA GTC ATG GAG CTC ATG GAT 336

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	Ser	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Ile	Val	Met	Glu	Leu	Met	Asp	
				100					105					110			
5	GCA	AAT	CTT	TGC	CAA	GTG	ATT	CAG	ATG	GAG	CTA	GAT	CAT	GAA	AGA	ATG	384
	Ala	Asn	Leu	Cys	Gln	Val	Ile	Gln	Met	Glu	Leu	Asp	His	Glu	Arg	Met	
			115					120					125				
10	TCC	TAC	CTT	CTC	TAT	CAG	ATG	CTG	TGT	GGA	ATC	AAG	CAC	CTT	CAT	TCT	432
	Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly	Ile	Lys	His	Leu	His	Ser	
			130				135					140					
15	GCT	GGA	ATT	ATT	CAT	CGG	GAC	TTA	AAG	CCC	AGT	AAT	ATA	GTA	GTA	AAA	480
	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Ile	Val	Val	Lys	
		145				150				155					160		
	TCT	GAT	TGC	ACT	TTG	AAG	ATT	CTT	GAC	TTC	GGT	CTG	GCC	AGG	ACT	GCA	
	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala	
				165					170						175		
20	GGA	ACG	AGT	TTT	ATG	ATG	ACG	CCT	TAT	GTA	GTG	ACT	CGC	TAC	TAC	AGA	576
	Gly	Thr	Ser	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg	
				180					185					190			
25	GCA	CCC	GAG	GTC	ATC	CTT	GGC	ATG	GGC	TAC	AAG	GAA	AAC	GTG	GAT	TTA	624
	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Leu	
			195					200					205				
30	TGG	TCT	GTG	GGG	TGC	ATT	ATG	GGA	GAA	ATG	GTT	TGC	CAC	AAA	ATC	CTC	672
	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Met	Val	Cys	His	Lys	Ile	Leu	
		210					215					220					
35	TTT	CCA	GGA	AGG	GAC	TAT	ATT	GAT	CAG	TGG	AAT	AAA	GTT	ATT	GAA	CAG	720
	Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln	
		225				230				235					240		
	CTT	GGA	ACA	CCA	TGT	CCT	GAA	TTC	ATG	AAG	AAA	CTG	CAA	CCA	ACA	GTA	
	Leu	Gly	Thr	Pro	Cys	Pro	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val	
				245					250						255		
40	AGG	ACT	TAC	GTT	GAA	AAC	AGA	CCT	AAA	TAT	GCT	GGA	TAT	AGC	TTT	GAG	816
	Arg	Thr	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Ala	Gly	Tyr	Ser	Phe	Glu	
				260					265					270			
45	AAA	CTC	TTC	CCT	GAT	GTC	CTT	TTC	CCA	GCT	GAC	TCA	GAA	CAC	AAC	AAA	864
	Lys	Leu	Phe	Pro	Asp	Val	Leu	Phe	Pro	Ala	Asp	Ser	Glu	His	Asn	Lys	
			275					280					285				
50	CTT	AAA	GCC	AGT	CAG	GCA	AGG	GAT	TTG	TTA	TCC	AAA	ATG	CTG	GTA	ATA	912
	Leu	Lys	Ala	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile	
		290					295					300					
55	GAT	GCA	TCT	AAA	AGG	ATC	TCT	GTA	GAT	GAA	GCT	CTC	CAA	CAC	CCG	TAC	960
	Asp	Ala	Ser	Lys	Arg	Ile	Ser	Val	Asp	Glu	Ala	Leu	Gln	His	Pro	Tyr	
		305				310				315					320		
	ATC	AAT	GTC	TGG	TAT	GAT	CCT	TCT	GAA	GCA	GAA	GCT	CCA	CCA	CCA	AAG	1008

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	Ile	Asn	Val	Trp	Tyr	Asp	Pro	Ser	Glu	Ala	Glu	Ala	Pro	Pro	Pro	Lys	
					325					330					335		
5	ATC	CCT	GAC	AAG	CAG	TTA	GAT	GAA	AGG	GAA	CAC	ACA	ATA	GAA	GAG	TGG	1056
	Ile	Pro	Asp	Lys	Gln	Leu	Asp	Glu	Arg	Glu	His	Thr	Ile	Glu	Glu	Trp	
				340					345					350			
10	AAA	GAA	TTG	ATA	TAT	AAG	GAA	GTT	ATG	GAC	TTG	GAG	GAG	AGA	ACC	AAG	1104
	Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asp	Leu	Glu	Glu	Arg	Thr	Lys	
			355					360					365				
15	AAT	GGA	GTT	ATA	CGG	GGG	CAG	CCC	TCT	CCT	TTA	GCA	CAG	GTG	CAG	CAG	1152
	Asn	Gly	Val	Ile	Arg	Gly	Gln	Pro	Ser	Pro	Leu	Ala	Gln	Val	Gln	Gln	
			370				375					380					
20	TGG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	1200
	Trp	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	
		385				390					395				400		
25	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	1248
	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	
					405					410					415		
30	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	1296
	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	
				420				425					430				
35	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	1344
	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	
			435				440						445				
40	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	1392
	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	
		450				455					460						
45	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	1440
	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	
		465				470				475					480		
50	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	1488
	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	
					485					490					495		
55	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	1536
	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	
				500					505					510			
60	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	1584
	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	
			515					520					525				
65	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	1632
	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	
		530					535					540					
70	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	1680

135

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Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg  
 545 550 555 560

5 CAC AAC ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG 1728  
 His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln  
 565 570 575

10 AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC 1776  
 Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr  
 580 585 590

15 CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT 1824  
 Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp  
 595 600 605

CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC 1872  
 His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly  
 610 615 620

20 ATG GAC GAG CTG TAC AAG TAA 1893  
 Met Asp Glu Leu Tyr Lys  
 625 630

25 (2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 630 amino acids  
 (B) TYPE: amino acid  
 30 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Ser Arg Ser Lys Arg Asp Asn Asn Phe Tyr Ser Val Glu Ile Gly  
 1 5 10 15  
 40 Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro Ile  
 20 25 30  
 Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Ile Leu  
 35 40 45  
 Glu Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln  
 45 50 55 60  
 Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys Val  
 65 70 75 80  
 Asn His Lys Asn Ile Ile Gly Leu Leu Asn Val Phe Thr Pro Gln Lys  
 85 90 95  
 50 Ser Leu Glu Glu Phe Gln Asp Val Tyr Ile Val Met Glu Leu Met Asp  
 100 105 110  
 Ala Asn Leu Cys Gln Val Ile Gln Met Glu Leu Asp His Glu Arg Met  
 115 120 125  
 Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu His Ser  
 55 130 135 140  
 Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys

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145                      150                      155                      160  
 Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr Ala  
                                  165                      170                      175  
 5 Gly Thr Ser Phe Met Met Thr Pro Tyr Val Val Thr Arg Tyr Tyr Arg  
                                  180                      185                      190  
 Ala Pro Glu Val Ile Leu Gly Met Gly Tyr Lys Glu Asn Val Asp Leu  
                                  195                      200                      205  
 Trp Ser Val Gly Cys Ile Met Gly Glu Met Val Cys His Lys Ile Leu  
                                  210                      215                      220  
 10 Phe Pro Gly Arg Asp Tyr Ile Asp Gln Trp Asn Lys Val Ile Glu Gln  
                                  225                      230                      235                      240  
 Leu Gly Thr Pro Cys Pro Glu Phe Met Lys Lys Leu Gln Pro Thr Val  
                                  245                      250                      255  
 15 Arg Thr Tyr Val Glu Asn Arg Pro Lys Tyr Ala Gly Tyr Ser Phe Glu  
                                  260                      265                      270  
 Lys Leu Phe Pro Asp Val Leu Phe Pro Ala Asp Ser Glu His Asn Lys  
                                  275                      280                      285  
 Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu Ser Lys Met Leu Val Ile  
                                  290                      295                      300  
 20 Asp Ala Ser Lys Arg Ile Ser Val Asp Glu Ala Leu Gln His Pro Tyr  
                                  305                      310                      315                      320  
 Ile Asn Val Trp Tyr Asp Pro Ser Glu Ala Glu Ala Pro Pro Pro Lys  
                                  325                      330                      335  
 25 Ile Pro Asp Lys Gln Leu Asp Glu Arg Glu His Thr Ile Glu Glu Trp  
                                  340                      345                      350  
 Lys Glu Leu Ile Tyr Lys Glu Val Met Asp Leu Glu Glu Arg Thr Lys  
                                  355                      360                      365  
 Asn Gly Val Ile Arg Gly Gln Pro Ser Pro Leu Ala Gln Val Gln Gln  
                                  370                      375                      380  
 30 Trp Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe  
                                  385                      390                      395                      400  
 Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly  
                                  405                      410                      415  
 35 His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly  
                                  420                      425                      430  
 Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro  
                                  435                      440                      445  
 Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser  
                                  450                      455                      460  
 40 Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met  
                                  465                      470                      475                      480  
 Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly  
                                  485                      490                      495  
 45 Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val  
                                  500                      505                      510  
 Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile  
                                  515                      520                      525  
 Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile  
                                  530                      535                      540  
 50 Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg  
                                  545                      550                      555                      560  
 His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln  
                                  565                      570                      575  
 55 Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr  
                                  580                      585                      590  
 Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp

137

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His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly  
610 615 620

Met Asp Glu Leu Tyr Lys  
5 625 630

(2) INFORMATION FOR SEO ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1821 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 20 (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...1818  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:64:

25	ATG Met 1	TCT Ser	CAG Gln	GAG Glu	AGG Arg 5	CCC Pro	ACG Thr	TTC Phe	TAC Tyr 10	CGG Arg	CAG Gln	GAG Glu	CTG Leu	AAC Asn	AAG Lys 15	ACA Thr	48
30	ATC Ile	TGG Trp	GAG Glu	GTG Val 20	CCC Pro	GAG Glu	CGT Arg	TAC Tyr 25	CAG Gln	AAC Asn	CTG Leu	TCT Ser	CCA Pro	GTG Val 30	GGC Gly	TCT Ser	96
35	GGC Gly	GCC Ala	TAT Tyr 35	GGC Gly	TCT Ser	GTG Val	TGT Cys	GCT Ala 40	GCT Ala	TTT Phe	GAC Asp	ACA Thr	AAA Lys	ACG Thr	GGG Gly	TTA Leu	144
40	CGT Arg 50	GTG Val	GCA Ala	GTG Val	AAG Lys	AAG Lys	CTC Leu 55	TCC Ser	AGA Arg	CCA Pro	TTT Phe	CAG Gln 60	TCC Ser	ATC Ile	ATT Ile	CAT His	192
45	GCG Ala 65	AAA Lys	AGA Arg	ACC Thr	TAC Tyr	AGA Arg 70	GAA Glu	CTG Leu	CGG Arg	TTA Leu 75	CTT Leu	AAA Lys	CAT His	ATG Met	AAA Lys 80	CAT His	240
50	GAA Glu	AAT Asn	GTG Val	ATT Ile	GGT Gly 85	CTG Leu	TTG Leu	GAC Asp	GTT Val	TTT Phe 90	ACA Thr	CCT Pro	GCA Ala	AGG Arg	TCT Ser 95	CTG Leu	288
55	GAG Glu	GAA Glu	TTC Phe	AAT Asn	GAT Asp	GTG Val 100	TAT Tyr	CTG Leu	GTG Val 105	ACC Thr	CAT His	CTC Leu	ATG Met	GGG Gly 110	GCA Ala	GAT Asp	336
60	CTG Leu	AAC Asn	AAC Asn	ATT Ile	GTG Val	AAA Lys	TGT Cys	CAG Gln 120	AAG Lys	CTT Leu	ACA Thr	GAT Asp	GAC Asp	CAT His	GTT Val	CAG Gln	384
65	TTC Tyr	CTT Trp	ATC Ile	TAC Val	CAA Asn	ATT Tyr	CTC Leu	CGA Gln	GGT Val	CTA Leu	AAG Thr	TAT Asp	ATA Asp	CAT His	TCA Val	GCT Gln	432

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	Phe	Leu	Ile	Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	
	130						135					140					
5	GAC	ATA	ATT	CAC	AGG	GAC	CTA	AAA	CCT	AGT	AAT	CTA	GCT	GTG	AAT	GAA	480
	Asp	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Ala	Val	Asn	Glu	
	145					150					155					160	
10	GAC	TGT	GAG	CTG	AAG	ATT	CTG	GAT	TTT	GGA	CTG	GCT	CGG	CAC	ACA	GAT	528
	Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	His	Thr	Asp	
					165					170						175	
15	GAT	GAA	ATG	ACA	GGC	TAC	GTG	GCC	ACT	AGG	TGG	TAC	AGG	GCT	CCT	GAG	576
	Asp	Glu	Met	Thr	Gly	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	
					180					185						190	
20	ATC	ATG	CTG	AAC	TGG	ATG	CAT	TAC	AAC	CAG	ACA	GTT	GAT	ATT	TGG	TCA	624
	Ile	Met	Leu	Asn	Trp	Met	His	Tyr	Asn	Gln	Thr	Val	Asp	Ile	Trp	Ser	
			195					200						205			
25	GTG	GGA	TGC	ATA	ATG	GCC	GAG	CTG	TTG	ACT	GGA	AGA	ACA	TTG	TTT	CCT	672
	Val	Gly	Cys	Ile	Met	Ala	Glu	Leu	Leu	Thr	Gly	Arg	Thr	Leu	Phe	Pro	
		210					215						220				
30	GGT	ACA	GAC	CAT	ATT	GAT	CAG	TTG	AAG	CTC	ATT	TTA	AGA	CTC	GTT	GGA	720
	Gly	Thr	Asp	His	Ile	Asp	Gln	Leu	Lys	Leu	Ile	Leu	Arg	Leu	Val	Gly	
	225					230					235					240	
35	ACC	CCA	GGG	GCT	GAG	CTT	TTG	AAG	AAA	ATC	TCC	TCA	GAG	TCT	GCA	AGA	768
	Thr	Pro	Gly	Ala	Glu	Leu	Leu	Lys	Lys	Ile	Ser	Ser	Glu	Ser	Ala	Arg	
					245					250						255	
40	AAC	TAT	ATT	CAG	TCT	TTG	ACT	CAG	ATG	CCG	AAG	ATG	AAC	TTT	GCG	AAT	816
	Asn	Tyr	Ile	Gln	Ser	Leu	Thr	Gln	Met	Pro	Lys	Met	Asn	Phe	Ala	Asn	
				260						265					270		
45	GTA	TTT	ATT	GGT	GCC	AAT	CCC	CTG	GCT	GTC	GAC	TTG	CTG	GAG	AAG	ATG	864
	Val	Phe	Ile	Gly	Ala	Asn	Pro	Leu	Ala	Val	Asp	Leu	Leu	Glu	Lys	Met	
			275					280						285			
50	CTT	GTA	TTG	GAC	TCA	GAT	AAG	AGA	ATT	ACA	GCG	GCC	CAA	GCC	CTT	GCA	912
	Leu	Val	Leu	Asp	Ser	Asp	Lys	Arg	Ile	Thr	Ala	Ala	Gln	Ala	Leu	Ala	
		290					295						300				
55	CAT	GCC	TAC	TTT	GCT	CAG	TAC	CAC	GAT	CCT	GAT	GAT	GAA	CCA	GTG	GCC	960
	His	Ala	Tyr	Phe	Ala	Gln	Tyr	His	Asp	Pro	Asp	Asp	Glu	Pro	Val	Ala	
	305					310					315					320	
60	GAT	CCT	TAT	GAT	CAG	TCC	TTT	GAA	AGC	AGG	GAC	CTC	CTT	ATA	GAT	GAG	1008
	Asp	Pro	Tyr	Asp	Gln	Ser	Phe	Glu	Ser	Arg	Asp	Leu	Leu	Ile	Asp	Glu	
					325					330						335	
65	TGG	AAA	AGC	CTG	ACC	TAT	GAT	GAA	GTC	ATC	AGC	TTT	GTG	CCA	CCA	CCC	1056
	Trp	Lys	Ser	Leu	Thr	Tyr	Asp	Glu	Val	Ile	Ser	Phe	Val	Pro	Pro	Pro	
				340						345						350	
70	CTT	GAC	CAA	GAA	GAG	ATG	GAG	TCC	GAG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	1104

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	Leu	Asp	Gln	Glu	Glu	Met	Glu	Ser	Glu	Asp	Pro	Pro	Val	Ala	Thr	Met	
			355					360					365				
5	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	1152
	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
			370				375					380					
10	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	1200
	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
			385			390				395					400		
15	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	1248
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
				405					410					415			
20	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	1296
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
				420				425					430				
25	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	1344
	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	
			435				440					445					
30	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	1392
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
			450				455					460					
35	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	1440
	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			465			470				475					480		
40	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	1488
	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
				485					490					495			
45	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC	1536
	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
				500				505					510				
50	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC	1584
	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
			515				520					525					
55	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	GTG	1632
	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	
			530				535					540					
60	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	CCC	1680
	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	
			545			550				555					560		
65	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	AGC	1728
	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	
				565				570				575					
70	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	GTG	1776

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Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 580 585 590

ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA 1821  
 5 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 595 600 605

## (2) INFORMATION FOR SEQ ID NO:65:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr  
 1 5 10 15  
 Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser  
 25 20 25 30  
 Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly Leu  
 35 40 45  
 Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His  
 50 55 60  
 30 Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His  
 65 70 75 80  
 Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu  
 85 90 95  
 Glu Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp  
 35 100 105 110  
 Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln  
 115 120 125  
 Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala  
 130 135 140  
 40 Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu  
 145 150 155 160  
 Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp  
 165 170 175  
 Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu  
 45 180 185 190  
 Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser  
 195 200 205  
 Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro  
 210 215 220  
 50 Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly  
 225 230 235 240  
 Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg  
 245 250 255  
 Asn Tyr Ile Gln Ser Leu Thr Gln Met Pro Lys Met Asn Phe Ala Asn  
 55 260 265 270  
 Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met

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		275				280						285					
		Leu	Val	Leu	Asp	Ser	Asp	Lys	Arg	Ile	Thr	Ala	Ala	Gln	Ala	Leu	Ala
		290						295					300				
5		His	Ala	Tyr	Phe	Ala	Gln	Tyr	His	Asp	Pro	Asp	Asp	Glu	Pro	Val	Ala
		305					310					315				320	
		Asp	Pro	Tyr	Asp	Gln	Ser	Phe	Glu	Ser	Arg	Asp	Leu	Leu	Ile	Asp	Glu
						325					330					335	
		Trp	Lys	Ser	Leu	Thr	Tyr	Asp	Glu	Val	Ile	Ser	Phe	Val	Pro	Pro	Pro
					340					345				350			
10		Leu	Asp	Gln	Glu	Glu	Met	Glu	Ser	Glu	Asp	Pro	Pro	Val	Ala	Thr	Met
				355				360						365			
		Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
				370				375					380				
		Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
15				385			390					395				400	
		Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
					405						410					415	
		Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu
				420						425				430			
20		Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln
				435				440					445				
		His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
				450				455					460				
		Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
25				465			470					475				480	
		Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
					485					490						495	
		Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
				500						505				510			
30		Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
				515				520						525			
		Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val
				530				535					540				
		Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
35				545			550					555				560	
		Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
					565					570						575	
		Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
				580						585				590			
40		Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys		
				595				600						605			

(2) INFORMATION FOR SEQ ID NO:66:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2913 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: cDNA  
 (ix) FEATURE:
- 55 (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...2910  
 (D) OTHER INFORMATION:

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

5	ATG AGT GCT GAG GGG TAC CAG TAC AGA GCG CTG TAT GAT TAT AAA AAG	48
	Met Ser Ala Glu Gly Tyr Gln Tyr Arg Ala Leu Tyr Asp Tyr Lys Lys	
	1 5 10 15	
10	GAA AGA GAA GAA GAT ATT GAC TTG CAC TTG GGT GAC ATA TTG ACT GTG	96
	Glu Arg Glu Glu Asp Ile Asp Leu His Leu Gly Asp Ile Leu Thr Val	
	20 25 30	
15	AAT AAA GGG TCC TTA GTA GCT CTT GGA TTC AGT GAT GGA CAG GAA GCC	144
	Asn Lys Gly Ser Leu Val Ala Leu Gly Phe Ser Asp Gly Gln Glu Ala	
	35 40 45	
20	AGG CCT GAA GAA ATT GGC TGG TTA AAT GGC TAT AAT GAA ACC ACA GGG	192
	Arg Pro Glu Glu Ile Gly Trp Leu Asn Gly Tyr Asn Glu Thr Thr Gly	
	50 55 60	
25	GAA AGG GGG GAC TTT CCG GGA ACT TAC GTA GAA TAT ATT GGA AGG AAA	240
	Glu Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Tyr Ile Gly Arg Lys	
	65 70 75 80	
30	AAA ATC TCG CCT CCC ACA CCA AAG CCC CGG CCA CCT CGG CCT CTT CCT	288
	Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro Arg Pro Leu Pro	
	85 90 95	
35	GTT GCA CCA GGT TCT TCG AAA ACT GAA GCA GAT GTT GAA CAA CAA GCT	336
	Val Ala Pro Gly Ser Ser Lys Thr Glu Ala Asp Val Glu Gln Gln Ala	
	100 105 110	
40	TTG ACT CTC CCG GAT CTT GCA GAG CAG TTT GCC CCT CCT GAC ATT GCC	384
	Leu Thr Leu Pro Asp Leu Ala Glu Gln Phe Ala Pro Pro Asp Ile Ala	
	115 120 125	
45	CCG CCT CTT CTT ATC AAG CTC GTG GAA GCC ATT GAA AAG AAA GGT CTG	432
	Pro Pro Leu Leu Ile Lys Leu Val Glu Ala Ile Glu Lys Lys Gly Leu	
	130 135 140	
50	GAA TGT TCA ACT CTA TAC AGA ACA CAG AGC TCC AGC AAC CTG GCA GAA	480
	Glu Cys Ser Thr Leu Tyr Arg Thr Gln Ser Ser Ser Asn Leu Ala Glu	
	145 150 155 160	
55	TTA CGA CAG CTT CTT GAT TGT GAT ACA CCC TCC GTG GAC TTG GAA ATG	528
	Leu Arg Gln Leu Leu Asp Cys Asp Thr Pro Ser Val Asp Leu Glu Met	
	165 170 175	
60	ATC GAT GTG CAC GTT TTG GCT GAC GCT TTC AAA CGC TAT CTC CTG GAC	576
	Ile Asp Val His Val Leu Ala Asp Ala Phe Lys Arg Tyr Leu Leu Asp	
	180 185 190	
65	TTA CCA AAT CCT GTC ATT CCA GCA GCC GTT TAC AGT GAA ATG ATT TCT	624
	Leu Pro Asn Pro Val Ile Pro Ala Ala Val Tyr Ser Glu Met Ile Ser	
	195 200 205	
70	TTA GCT CCA GAA GTA CAA AGC TCC GAA GAA TAT ATT CAG CTA TTG AAG	672

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	Leu	Ala	Pro	Glu	Val	Gln	Ser	Ser	Glu	Glu	Tyr	Ile	Gln	Leu	Leu	Lys	
	210						215					220					
5	AAG	CTT	ATT	AGG	TCG	CCT	AGC	ATA	CCT	CAT	CAG	TAT	TGG	CTT	ACG	CTT	720
	Lys	Leu	Ile	Arg	Ser	Pro	Ser	Ile	Pro	His	Gln	Tyr	Trp	Leu	Thr	Leu	
	225					230					235					240	
10	CAG	TAT	TTG	TTA	AAA	CAT	TTC	TTC	AAG	CTC	TCT	CAA	ACC	TCC	AGC	AAA	768
	Gln	Tyr	Leu	Leu	Lys	His	Phe	Phe	Lys	Leu	Ser	Gln	Thr	Ser	Ser	Lys	
					245					250					255		
15	AAT	CTG	TTG	AAT	GCA	AGA	GTA	CTC	TCT	GAA	ATT	TTC	AGC	CCT	ATG	CTT	816
	Asn	Leu	Leu	Asn	Ala	Arg	Val	Leu	Ser	Glu	Ile	Phe	Ser	Pro	Met	Leu	
				260					265					270			
	TTC	AGA	TTC	TCA	GCA	GCC	AGC	TCT	GAT	AAT	ACT	GAA	AAC	CTC	ATA	AAA	864
	Phe	Arg	Phe	Ser	Ala	Ala	Ser	Ser	Asp	Asn	Thr	Glu	Asn	Leu	Ile	Lys	
				275				280					285				
20	GTT	ATA	GAA	ATT	TTA	ATC	TCA	ACT	GAA	TGG	AAT	GAA	CGA	CAG	CCT	GCA	912
	Val	Ile	Glu	Ile	Leu	Ile	Ser	Thr	Glu	Trp	Asn	Glu	Arg	Gln	Pro	Ala	
		290					295					300					
25	CCA	GCA	CTG	CCT	CCT	AAA	CCA	CCA	AAA	CCT	ACT	ACT	GTA	GCC	AAC	AAC	960
	Pro	Ala	Leu	Pro	Pro	Lys	Pro	Pro	Lys	Pro	Thr	Thr	Val	Ala	Asn	Asn	
	305					310					315					320	
30	GGT	ATG	AAT	AAC	AAT	ATG	TCC	TTA	CAA	AAT	GCT	GAA	TGG	TAC	TGG	GGA	1008
	Gly	Met	Asn	Asn	Asn	Met	Ser	Leu	Gln	Asn	Ala	Glu	Trp	Tyr	Trp	Gly	
					325					330					335		
35	GAT	ATC	TCG	AGG	GAA	GAA	GTG	AAT	GAA	AAA	CTT	CGA	GAT	ACA	GCA	GAC	1056
	Asp	Ile	Ser	Arg	Glu	Glu	Val	Asn	Glu	Lys	Leu	Arg	Asp	Thr	Ala	Asp	
				340					345					350			
	GGG	ACC	TTT	TTG	GTA	CGA	GAT	GCG	TCT	ACT	AAA	ATG	CAT	GGT	GAT	TAT	1104
	Gly	Thr	Phe	Leu	Val	Arg	Asp	Ala	Ser	Thr	Lys	Met	His	Gly	Asp	Tyr	
				355				360					365				
40	ACT	CTT	ACA	CTA	AGG	AAA	GGG	GGA	AAT	AAC	AAA	TTA	ATC	AAA	ATA	TTT	1152
	Thr	Leu	Thr	Leu	Arg	Lys	Gly	Gly	Asn	Asn	Lys	Leu	Ile	Lys	Ile	Phe	
		370					375					380					
45	CAT	CGA	GAT	GGG	AAA	TAT	GGC	TTC	TCT	GAC	CCA	TTA	ACC	TTC	AGT	TCT	1200
	His	Arg	Asp	Gly	Lys	Tyr	Gly	Phe	Ser	Asp	Pro	Leu	Thr	Phe	Ser	Ser	
	385					390					395					400	
50	GTG	GTT	GAA	TTA	ATA	AAC	CAC	TAC	CGG	AAT	GAA	TCT	CTA	GCT	CAG	TAT	1248
	Val	Val	Glu	Leu	Ile	Asn	His	Tyr	Arg	Asn	Glu	Ser	Leu	Ala	Gln	Tyr	
					405					410					415		
55	AAT	CCC	AAA	TTG	GAT	GTG	AAA	TTA	CTT	TAT	CCA	GTA	TCC	AAA	TAC	CAA	1296
	Asn	Pro	Lys	Leu	Asp	Val	Lys	Leu	Leu	Tyr	Pro	Val	Ser	Lys	Tyr	Gln	
				420					425					430			
	CAG	GAT	CAA	GTT	GTC	AAA	GAA	GAT	AAT	ATT	GAA	GCT	GTA	GGG	AAA	AAA	1344

144

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	Gln Asp Gln Val Val Lys Glu Asp Asn Ile Glu Ala Val Gly Lys Lys	
	435 440 445	
5	TTA CAT GAA TAT AAC ACT CAG TTT CAA GAA AAA AGT CGA GAA TAT GAT Leu His Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser Arg Glu Tyr Asp	1392
	450 455 460	
10	AGA TTA TAT GAA GAA TAT ACC CGC ACA TCC CAG GAA ATC CAA ATG AAA Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu Ile Gln Met Lys	1440
	465 470 475 480	
15	AGG ACA GCT ATT GAA GCA TTT AAT GAA ACC ATA AAA ATA TTT GAA GAA Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu Glu	1488
	485 490 495	
20	CAG TGC CAG ACC CAA GAG CGG TAC AGC AAA GAA TAC ATA GAA AAG TTT Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr Ile Glu Lys Phe	1536
	500 505 510	
25	AAA CGT GAA GGC AAT GAG AAA GAA ATA CAA AGG ATT ATG CAT AAT TAT Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile Met His Asn Tyr	1584
	515 520 525	
30	GAT AAG TTG AAG TCT CGA ATC AGT GAA ATT ATT GAC AGT AGA AGA AGA Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp Ser Arg Arg Arg	1632
	530 535 540	
35	TTG GAA GAA GAC TTG AAG AAG CAG GCA GCT GAG TAT CGA GAA ATT GAC Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr Arg Glu Ile Asp	1680
	545 550 555 560	
40	AAA CGT ATG AAC AGC ATT AAA CCA GAC CTT ATC CAG CTG AGA AAG ACG Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln Leu Arg Lys Thr	1728
	565 570 575	
45	AGA GAC CAA TAC TTG ATG TGG TTG ACT CAA AAA GGT GTT CGG CAA AAG Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly Val Arg Gln Lys	1776
	580 585 590	
50	AAG TTG AAC GAG TGG TTG GGC AAT GAA AAC ACT GAA GAC CAA TAT TCA Lys Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu Asp Gln Tyr Ser	1824
	595 600 605	
55	CTG GTG GAA GAT GAT GAA GAT TTG CCC CAT CAT GAT GAG AAG ACA TGG Leu Val Glu Asp Asp Glu Asp Leu Pro His His Asp Glu Lys Thr Trp	1872
	610 615 620	
60	AAT GTT GGA AGC AGC AAC CGA AAC AAA GCT GAA AAC CTG TTG CGA GGG Asn Val Gly Ser Ser Asn Arg Asn Lys Ala Glu Asn Leu Leu Arg Gly	1920
	625 630 635 640	
65	AAG CGA GAT GGC ACT TTT CTT GTC CGG GAG AGC AGT AAA CAG GGC TGC Lys Arg Asp Gly Thr Phe Leu Val Arg Glu Ser Ser Lys Gln Gly Cys	1968
	645 650 655	
70	TAT GCC TGC TCT GTA GTG GTG GAC GGC GAA GTA AAG CAT TGT GTC ATA	2016

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	Tyr	Ala	Cys	Ser	Val	Val	Val	Asp	Gly	Glu	Val	Lys	His	Cys	Val	Ile	
				660					665					670			
5	AAC	AAA	ACA	GCA	ACT	GGC	TAT	GGC	TTT	GCC	GAG	CCC	TAT	AAC	TTG	TAC	2064
	Asn	Lys	Thr	Ala	Thr	Gly	Tyr	Gly	Phe	Ala	Glu	Pro	Tyr	Asn	Leu	Tyr	
			675					680					685				
10	AGC	TCT	CTG	AAA	GAA	CTG	GTG	CTA	CAT	TAC	CAA	CAC	ACC	TCC	CTT	GTG	2112
	Ser	Ser	Leu	Lys	Glu	Leu	Val	Leu	His	Tyr	Gln	His	Thr	Ser	Leu	Val	
			690				695					700					
15	CAG	CAC	AAC	GAC	TCC	CTC	AAT	GTC	ACA	CTA	GCC	TAC	CCA	GTA	TAT	GCA	2160
	Gln	His	Asn	Asp	Ser	Leu	Asn	Val	Thr	Leu	Ala	Tyr	Pro	Val	Tyr	Ala	
	705					710					715					720	
20	CAG	CAG	AGG	CGA	CAG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GTG	AGC	AAG	GGC	2208
	Gln	Gln	Arg	Arg	Gln	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	
					725					730					735		
25	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	GAC	GGC	2256
	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	
				740					745					750			
30	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	GAG	GGC	GAT	2304
	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	
			755					760				765					
35	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	AAG	2352
	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	
			770				775					780					
40	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	ACC	TAC	GGC	GTG	2400
	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	
	785					790					795				800		
45	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	CAC	GAC	TTC	TTC	2448
	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	
					805					810					815		
50	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC	TTC	TTC	2496
	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	
				820					825					830			
55	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	TTC	GAG	GGC	2544
	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	
			835					840					845				
60	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	GAG	2592
	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	
			850				855					860					
65	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC	TAC	AAC	AGC	CAC	2640
	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	
	865					870					875					880	
70	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC	ATC	AAG	GTG	AAC	2688

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Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn  
885 890 895

5 TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC 2736  
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp  
900 905 910

10 CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC 2784  
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
915 920 925

GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC 2832  
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
930 935 940

15 GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG 2880  
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
945 950 955 960

20 ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA 2913  
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
965 970

25 (2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 970 amino acids  
(B) TYPE: amino acid  
30 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Ser Ala Glu Gly Tyr Gln Tyr Arg Ala Leu Tyr Asp Tyr Lys Lys  
1 5 10 15  
40 Glu Arg Glu Glu Asp Ile Asp Leu His Leu Gly Asp Ile Leu Thr Val  
20 25 30  
Asn Lys Gly Ser Leu Val Ala Leu Gly Phe Ser Asp Gly Gln Glu Ala  
35 40 45  
Arg Pro Glu Glu Ile Gly Trp Leu Asn Gly Tyr Asn Glu Thr Thr Gly  
50 55 60  
45 Glu Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Tyr Ile Gly Arg Lys  
65 70 75 80  
Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro Arg Pro Leu Pro  
85 90 95  
50 Val Ala Pro Gly Ser Ser Lys Thr Glu Ala Asp Val Glu Gln Gln Ala  
100 105 110  
Leu Thr Leu Pro Asp Leu Ala Glu Gln Phe Ala Pro Pro Asp Ile Ala  
115 120 125  
Pro Pro Leu Leu Ile Lys Leu Val Glu Ala Ile Glu Lys Lys Gly Leu  
130 135 140  
55 Glu Cys Ser Thr Leu Tyr Arg Thr Gln Ser Ser Ser Asn Leu Ala Glu

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	145		150		155		160
	Leu Arg Gln Leu Leu Asp Cys Asp Thr Pro Ser Val Asp Leu Glu Met						
		165		170			175
	Ile Asp Val His Val Leu Ala Asp Ala Phe Lys Arg Tyr Leu Leu Asp						
5		180		185			190
	Leu Pro Asn Pro Val Ile Pro Ala Ala Val Tyr Ser Glu Met Ile Ser						
		195		200			205
	Leu Ala Pro Glu Val Gln Ser Ser Glu Glu Tyr Ile Gln Leu Leu Lys						
		210		215			220
10	Lys Leu Ile Arg Ser Pro Ser Ile Pro His Gln Tyr Trp Leu Thr Leu						
		225		230			235
	Gln Tyr Leu Leu Lys His Phe Phe Lys Leu Ser Gln Thr Ser Ser Lys						
		245		250			255
	Asn Leu Leu Asn Ala Arg Val Leu Ser Glu Ile Phe Ser Pro Met Leu						
15		260		265			270
	Phe Arg Phe Ser Ala Ala Ser Ser Asp Asn Thr Glu Asn Leu Ile Lys						
		275		280			285
	Val Ile Glu Ile Leu Ile Ser Thr Glu Trp Asn Glu Arg Gln Pro Ala						
		290		295			300
20	Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Thr Thr Val Ala Asn Asn						
		305		310			315
	Gly Met Asn Asn Asn Met Ser Leu Gln Asn Ala Glu Trp Tyr Trp Gly						
		325		330			335
	Asp Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg Asp Thr Ala Asp						
25		340		345			350
	Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met His Gly Asp Tyr						
		355		360			365
	Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu Ile Lys Ile Phe						
		370		375			380
30	His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu Thr Phe Ser Ser						
		385		390			395
	Val Val Glu Leu Ile Asn His Tyr Arg Asn Glu Ser Leu Ala Gln Tyr						
		405		410			415
	Asn Pro Lys Leu Asp Val Lys Leu Leu Tyr Pro Val Ser Lys Tyr Gln						
35		420		425			430
	Gln Asp Gln Val Val Lys Glu Asp Asn Ile Glu Ala Val Gly Lys Lys						
		435		440			445
	Leu His Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser Arg Glu Tyr Asp						
		450		455			460
40	Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu Ile Gln Met Lys						
		465		470			475
	Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu Glu						
		485		490			495
	Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr Ile Glu Lys Phe						
45		500		505			510
	Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile Met His Asn Tyr						
		515		520			525
	Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp Ser Arg Arg Arg						
		530		535			540
50	Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr Arg Glu Ile Asp						
		545		550			555
	Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln Leu Arg Lys Thr						
		565		570			575
	Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly Val Arg Gln Lys						
55		580		585			590
	Lys Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu Asp Gln Tyr Ser						

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		595				600				605						
	Leu	Val	Glu	Asp	Asp	Glu	Asp	Leu	Pro	His	His	Asp	Glu	Lys	Thr	Trp
	610					615						620				
5	Asn	Val	Gly	Ser	Ser	Asn	Arg	Asn	Lys	Ala	Glu	Asn	Leu	Leu	Arg	Gly
	625					630					635				640	
	Lys	Arg	Asp	Gly	Thr	Phe	Leu	Val	Arg	Glu	Ser	Ser	Lys	Gln	Gly	Cys
					645					650					655	
	Tyr	Ala	Cys	Ser	Val	Val	Val	Asp	Gly	Glu	Val	Lys	His	Cys	Val	Ile
			660					665					670			
10	Asn	Lys	Thr	Ala	Thr	Gly	Tyr	Gly	Phe	Ala	Glu	Pro	Tyr	Asn	Leu	Tyr
			675					680					685			
	Ser	Ser	Leu	Lys	Glu	Leu	Val	Leu	His	Tyr	Gln	His	Thr	Ser	Leu	Val
			690					695				700				
15	Gln	His	Asn	Asp	Ser	Leu	Asn	Val	Thr	Leu	Ala	Tyr	Pro	Val	Tyr	Ala
	705					710					715				720	
	Gln	Gln	Arg	Arg	Gln	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly
					725						730				735	
	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly
			740					745					750			
20	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp
			755					760					765			
	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys
			770					775					780			
25	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val
	785					790					795				800	
	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe
					805					810					815	
	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe
			820					825					830			
30	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly
			835					840					845			
	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu
			850					855					860			
35	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His
	865					870					875				880	
	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn
					885					890					895	
	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp
			900					905					910			
40	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro
			915					920					925			
	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn
			930					935					940			
45	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly
	945					950					955				960	
	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys						
					965					970						

(2) INFORMATION FOR SEQ ID NO:68:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1788 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

55

(D) TOPOLOGY: linear

150

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1785

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

10	ATG GGC AAC GCC GCC GCC GCC AAG AAG GGC AGC GAG CAG GAG AGC GTG	48
	Met Gly Asn Ala Ala Ala Ala Lys Lys Gly Ser Glu Gln Glu Ser Val	
	1 5 10 15	
15	AAA GAG TTC CTA GCC AAA GCC AAG GAA GAT TTC CTG AAA AAA TGG GAA	96
	Lys Glu Phe Leu Ala Lys Ala Lys Glu Asp Phe Leu Lys Lys Trp Glu	
	20 25 30	
20	GAC CCC TCT CAG AAT ACA GCC CAG TTG GAT CAG TTT GAT AGA ATC AAG	144
	Asp Pro Ser Gln Asn Thr Ala Gln Leu Asp Gln Phe Asp Arg Ile Lys	
	35 40 45	
25	ACC CTT GGC ACC GGC TCC TTT GGG CGA GTG ATG CTG GTG AAG CAC AAG	192
	Thr Leu Gly Thr Gly Ser Phe Gly Arg Val Met Leu Val Lys His Lys	
	50 55 60	
30	GAG AGT GGG AAC CAC TAC GCC ATG AAG ATC TTA GAC AAG CAG AAG GTG	240
	Glu Ser Gly Asn His Tyr Ala Met Lys Ile Leu Asp Lys Gln Lys Val	
	65 70 75 80	
35	GTG AAG CTA AAG CAG ATC GAG CAC ACT CTG AAT GAG AAG CGC ATC CTG	288
	Val Lys Leu Lys Gln Ile Glu His Thr Leu Asn Glu Lys Arg Ile Leu	
	85 90 95	
40	CAG GCC GTC AAC TTC CCG TTC CTG GTC AAA CTT GAA TTC TCC TTC AAG	336
	Gln Ala Val Asn Phe Pro Phe Leu Val Lys Leu Glu Phe Ser Phe Lys	
	100 105 110	
45	GAC AAC TCA AAC CTG TAC ATG GTC ATG GAG TAT GTA GCT GGT GGC GAG	384
	Asp Asn Ser Asn Leu Tyr Met Val Met Glu Tyr Val Ala Gly Gly Glu	
	115 120 125	
50	ATG TTC TCC CAC CTA CGG CGG ATT GGA AGG TTC AGC GAG CCC CAT GCC	432
	Met Phe Ser His Leu Arg Arg Ile Gly Arg Phe Ser Glu Pro His Ala	
	130 135 140	
55	CGT TTC TAC GCG GCG CAG ATC GTC CTG ACC TTT GAG TAT CTG CAC TCC	480
	Arg Phe Tyr Ala Ala Gln Ile Val Leu Thr Phe Glu Tyr Leu His Ser	
	145 150 155 160	
60	CTG GAC CTC ATC TAC CGG GAC CTG AAG CCC GAG AAT CTT CTC ATC GAC	528
	Leu Asp Leu Ile Tyr Arg Asp Leu Lys Pro Glu Asn Leu Leu Ile Asp	
	165 170 175	
65	CAG CAG GGC TAT ATT CAG GTG ACA GAC TTC GGT TTT GCC AAG CGT GTG	576
	Gln Gln Gly Tyr Ile Gln Val Thr Asp Phe Gly Phe Ala Lys Arg Val	
	180 185 190	

150

151

	AAA GGC CGT ACT TGG ACC TTG TGT GGG ACC CCT GAG TAC TTG GCC CCC	624
	Lys Gly Arg Thr Trp Thr Leu Cys Gly Thr Pro Glu Tyr Leu Ala Pro	
	195 200 205	
5	GAG ATT ATC CTG AGC AAA GGC TAC AAC AAG GCT GTG GAC TGG TGG GCT	672
	Glu Ile Ile Leu Ser Lys Gly Tyr Asn Lys Ala Val Asp Trp Trp Ala	
	210 215 220	
10	CTC GGA GTC CTC ATC TAC GAG ATG GCT GCT GGT TAC CCA CCC TTC TTC	720
	Leu Gly Val Leu Ile Tyr Glu Met Ala Ala Gly Tyr Pro Pro Phe Phe	
	225 230 235 240	
15	GCT GAC CAG CCT ATC CAG ATC TAT GAG AAA ATC GTC TCT GGG AAG GTG	768
	Ala Asp Gln Pro Ile Gln Ile Tyr Glu Lys Ile Val Ser Gly Lys Val	
	245 250 255	
20	CGG TTC CCA TCC CAC TTC AGC TCT GAC TTG AAG GAC CTG CTG CGG AAC	816
	Arg Phe Pro Ser His Phe Ser Ser Asp Leu Lys Asp Leu Leu Arg Asn	
	260 265 270	
25	CTT CTG CAA GTG GAT CTA ACC AAG CGC TTT GGA AAC CTC AAG GAC GGG	864
	Leu Leu Gln Val Asp Leu Thr Lys Arg Phe Gly Asn Leu Lys Asp Gly	
	275 280 285	
30	GTC AAT GAC ATC AAG AAC CAC AAG TGG TTT GCC ACG ACT GAC TGG ATT	912
	Val Asn Asp Ile Lys Asn His Lys Trp Phe Ala Thr Thr Asp Trp Ile	
	290 295 300	
35	GCC ATC TAT CAG AGA AAG GTG GAA GCT CCC TTC ATA CCA AAG TTT AAA	960
	Ala Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Lys	
	305 310 315 320	
40	GGC CCT GGG GAC ACG AGT AAC TTT GAC GAC TAT GAG GAG GAA GAG ATC	1008
	Gly Pro Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Glu Ile	
	325 330 335	
45	CGG GTC TCC ATC AAT GAG AAG TGT GGC AAG GAG TTT ACT GAG TTT GGG	1056
	Arg Val Ser Ile Asn Glu Lys Cys Gly Lys Glu Phe Thr Glu Phe Gly	
	340 345 350	
50	CGC GCC ATG AGT AAA GGA GAA GAA CTT TTC ACT GGA GTT GTC CCA ATT	1104
	Arg Ala Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile	
	355 360 365	
55	CTT GTT GAA TTA GAT GGC GAT GTT AAT GGG CAA AAA TTC TCT GTT AGT	1152
	Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser	
	370 375 380	
60	GGA GAG GGT GAA GGT GAT GCA ACA TAC GGA AAA CTT ACC CTT AAA TTT	1200
	Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe	
	385 390 395 400	
65	ATT TGC ACT ACT GGG AAG CTA CCT GTT CCA TGG CCA ACG CTT GTC ACT	1248
	Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr	
	405 410 415	

151

152

	ACT CTC ACT TAT GGT GTT CAA TGC TTT TCT AGA TAC CCA GAT CAT ATG	1296
	Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met	
	420 425 430	
5	AAA CAG CAT GAC TTT TTC AAG AGT GCC ATG CCC GAA GGT TAT GTA CAG	1344
	Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln	
	435 440 445	
10	GAA AGA ACT ATA TTT TAC AAA GAT GAC GGG AAC TAC AAG ACA CGT GCT	1392
	Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala	
	450 455 460	
15	GAA GTC AAG TTT GAA GGT GAT ACC CTT GTT AAT AGA ATC GAG TTA AAA	1440
	Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys	
	465 470 475 480	
20	GGT ATT GAT TTT AAA GAA GAT GGA AAC ATT CTT GGA CAC AAA ATG GAA	1488
	Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu	
	485 490 495	
25	TAC AAT TAT AAC TCA CAT AAT GTA TAC ATC ATG GCA GAC AAA CCA AAG	1536
	Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys	
	500 505 510	
30	AAT GGC ATC AAA GTT AAC TTC AAA ATT AGA CAC AAC ATT AAA GAT GGA	1584
	Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly	
	515 520 525	
35	AGC GTT CAA TTA GCA GAC CAT TAT CAA CAA AAT ACT CCA ATT GGC GAT	1632
	Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
	530 535 540	
40	GGC CCT GTC CTT TTA CCA GAC AAC CAT TAC CTG TCC ACG CAA TCT GCC	1680
	Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala	
	545 550 555 560	
45	CTT TCC AAA GAT CCC AAC GAA AAG AGA GAT CAC ATG ATC CTT CTT GAG	1728
	Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu	
	565 570 575	
50	TTT GTA ACA GCT GCT GGG ATT ACA CAT GGC ATG GAT GAA CTA TAC AAA	1776
	Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys	
	580 585 590	
55	CCT CAG GAG TAA	1788
	Pro Gln Glu	
	595	

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 595 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

152

153

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

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Met Gly Asn Ala Ala Ala Lys Lys Gly Ser Glu Gln Glu Ser Val
 1           5           10           15
10 Lys Glu Phe Leu Ala Lys Ala Lys Glu Asp Phe Leu Lys Lys Trp Glu
    20           25           30
   Asp Pro Ser Gln Asn Thr Ala Gln Leu Asp Gln Phe Asp Arg Ile Lys
    35           40           45
   Thr Leu Gly Thr Gly Ser Phe Gly Arg Val Met Leu Val Lys His Lys
15    50           55           60
   Glu Ser Gly Asn His Tyr Ala Met Lys Ile Leu Asp Lys Gln Lys Val
   65           70           75           80
   Val Lys Leu Lys Gln Ile Glu His Thr Leu Asn Glu Lys Arg Ile Leu
    85           90           95
20 Gln Ala Val Asn Phe Pro Phe Leu Val Lys Leu Glu Phe Ser Phe Lys
    100           105           110
   Asp Asn Ser Asn Leu Tyr Met Val Met Glu Tyr Val Ala Gly Gly Glu
    115           120           125
   Met Phe Ser His Leu Arg Arg Ile Gly Arg Phe Ser Glu Pro His Ala
25    130           135           140
   Arg Phe Tyr Ala Ala Gln Ile Val Leu Thr Phe Glu Tyr Leu His Ser
   145           150           155           160
   Leu Asp Leu Ile Tyr Arg Asp Leu Lys Pro Glu Asn Leu Leu Ile Asp
    165           170           175
30 Gln Gln Gly Tyr Ile Gln Val Thr Asp Phe Gly Phe Ala Lys Arg Val
    180           185           190
   Lys Gly Arg Thr Trp Thr Leu Cys Gly Thr Pro Glu Tyr Leu Ala Pro
    195           200           205
   Glu Ile Ile Leu Ser Lys Gly Tyr Asn Lys Ala Val Asp Trp Trp Ala
35    210           215           220
   Leu Gly Val Leu Ile Tyr Glu Met Ala Ala Gly Tyr Pro Pro Phe Phe
   225           230           235           240
   Ala Asp Gln Pro Ile Gln Ile Tyr Glu Lys Ile Val Ser Gly Lys Val
    245           250           255
40 Arg Phe Pro Ser His Phe Ser Ser Asp Leu Lys Asp Leu Leu Arg Asn
    260           265           270
   Leu Leu Gln Val Asp Leu Thr Lys Arg Phe Gly Asn Leu Lys Asp Gly
    275           280           285
   Val Asn Asp Ile Lys Asn His Lys Trp Phe Ala Thr Thr Asp Trp Ile
45    290           295           300
   Ala Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Lys
   305           310           315           320
   Gly Pro Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Glu Ile
    325           330           335
50 Arg Val Ser Ile Asn Glu Lys Cys Gly Lys Glu Phe Thr Glu Phe Gly
    340           345           350
   Arg Ala Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
    355           360           365
   Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
55    370           375           380
   Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe

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153

154

385                      390                      395                      400  
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr  
                                  405                      410                      415  
 5    Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met  
                                  420                      425                      430  
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln  
                                  435                      440                      445  
 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala  
                                  450                      455                      460  
 10   Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys  
                                  465                      470                      475                      480  
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu  
                                  485                      490                      495  
 15   Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys  
                                  500                      505                      510  
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly  
                                  515                      520                      525  
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp  
                                  530                      535                      540  
 20   Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala  
                                  545                      550                      555                      560  
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu  
                                  565                      570                      575  
 25   Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
                                  580                      585                      590  
 Pro Gln Glu  
                                  595

## (2) INFORMATION FOR SEQ ID NO:70:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2181 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

40

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2178

(D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

45

ATG AGC GAC GTG GCT ATT GTG AAG GAG GGT TGG CTG CAC AAA CGA GGG      48  
 Met Ser Asp Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly  
   1                      5                      10                      15

50

GAG TAC ATC AAG ACC TGG CGG CCA CGC TAC TTC CTC CTC AAG AAT GAT      96  
 Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp  
                                  20                      25                      30

55

GGC ACC TTC ATT GGC TAC AAG GAG CGG CCG CAG GAT GTG GAC CAA CGT      144  
 Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg  
                                  35                      40                      45

154

155

	GAG GCT CCC CTC AAC AAC TTC TCT GTG GCG CAG TGC CAG CTG ATG AAG	192
	Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys	
	50 55 60	
5	ACG GAG CGG CCC CGG CCC AAC ACC TTC ATC ATC CGC TGC CTG CAG TGG	240
	Thr Glu Arg Pro Arg Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp	
	65 70 75 80	
10	ACC ACT GTC ATC GAA CGC ACC TTC CAT GTG GAG ACT CCT GAG GAG CGG	288
	Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg	
	85 90 95	
15	GAG GAG TGG ACA ACC GCC ATC CAG ACT GTG GCT GAC GGC CTC AAG AAG	336
	Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala Asp Gly Leu Lys Lys	
	100 105 110	
20	CAG GAG GAG GAG GAG ATG GAC TTC CGG TCG GGC TCA CCC AGT GAC AAC	384
	Gln Glu Glu Glu Glu Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn	
	115 120 125	
	TCA GGG GCT GAA GAG ATG GAG GTG TCC CTG GCC AAG CCC AAG CAC CGC	432
	Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys His Arg	
	130 135 140	
25	GTG ACC ATG AAC GAG TTT GAG TAC CTG AAG CTG CTG GGC AAG GGC ACT	480
	Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr	
	145 150 155 160	
30	TTC GGC AAG GTG ATC CTG GTG AAG GAG AAG GCC ACA GGC CGC TAC TAC	528
	Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr	
	165 170 175	
35	GCC ATG AAG ATC CTC AAG AAG GAA GTC ATC GTG GCC AAG GAC GAG GTG	576
	Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val	
	180 185 190	
40	GCC CAC ACA CTC ACC GAG AAC CGC GTC CTG CAG AAC TCC AGG CAC CCC	624
	Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro	
	195 200 205	
	TTC CTC ACA GCC CTG AAG TAC TCT TTC CAG ACC CAC GAC CGC CTC TGC	672
	Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys	
	210 215 220	
45	TTT GTC ATG GAG TAC GCC AAC GGG GGC GAG CTG TTC TTC CAC CTG TCC	720
	Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser	
	225 230 235 240	
50	CGG GAA CGT GTG TTC TCC GAG GAC CGG GCC CGC TTC TAT GGC GCT GAG	768
	Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu	
	245 250 255	
55	ATT GTG TCA GCC CTG GAC TAC CTG CAC TCG GAG AAG AAC GTG GTG TAC	816
	Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr	
	260 265 270	

155

156

	CGG GAC CTC AAG CTG GAG AAC CTC ATG CTG GAC AAG GAC GGG CAC ATT	864
	Arg Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile	
	275 280 285	
5	AAG ATC ACA GAC TTC GGG CTG TGC AAG GAG GGG ATC AAG GAC GGT GCC	912
	Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala	
	290 295 300	
10	ACC ATG AAG ACC TTT TGC GGC ACA CCT GAG TAC CTG GCC CCC GAG GTG	960
	Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val	
	305 310 315 320	
15	CTG GAG GAC AAT GAC TAC GGC CGT GCA GTG GAC TGG TGG GGG CTG GGC	1008
	Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly	
	325 330 335	
20	GTG GTC ATG TAC GAG ATG ATG TGC GGT CGC CTG CCC TTC TAC AAC CAG	1056
	Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln	
	340 345 350	
25	GAC CAT GAG AAG CTT TTT GAG CTC ATC CTC ATG GAG GAG ATC CGC TTC	1104
	Asp His Glu Lys Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg Phe	
	355 360 365	
30	CCG CGC ACG CTT GGT CCC GAG GCC AAG TCC TTG CTT TCA GGG CTG CTC	1152
	Pro Arg Thr Leu Gly Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu	
	370 375 380	
35	AAG AAG GAC CCC AAG CAG AGG CTT GGC GGG GGC TCC GAG GAC GCC AAG	1200
	Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Gly Ser Glu Asp Ala Lys	
	385 390 395 400	
40	GAG ATC ATG CAG CAT CGC TTC TTT GCC GGT ATC GTG TGG CAG CAC GTG	1248
	Glu Ile Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His Val	
	405 410 415	
45	TAC GAG AAG AAG CTC AGC CCA CCC TTC AAG CCC CAG GTC ACG TCG GAG	1296
	Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser Glu	
	420 425 430	
50	ACT GAC ACC AGG TAT TTT GAT GAG GAG TTC ACG GCC CAG ATG ATC ACC	1344
	Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr	
	435 440 445	
55	ATC ACA CCA CCT GAC CAA GAT GAC AGC ATG GAG TGT GTG GAC AGC GAG	1392
	Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser Glu	
	450 455 460	
60	CGC AGG CCC CAC TTC CCC CAG TTC TCC TAC TCG GCC AGC AGC ACG GCC	1440
	Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ser Thr Ala	
	465 470 475 480	
65	TCG GAT CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC	1488
	Ser Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe	
	485 490 495	

156



157

5	ACC GGG GTG GTG CCC ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC	1536
	Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly	
	500 505 510	
10	CAC AAG TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC	1584
	His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly	
	515 520 525	
15	AAG CTG ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC	1632
	Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro	
	530 535 540	
20	TGG CCC ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC	1680
	Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser	
	545 550 555 560	
25	CGC TAC CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG	1728
	Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met	
	565 570 575	
30	CCC GAA GGC TAC GTC CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC	1776
	Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly	
	580 585 590	
35	AAC TAC AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG	1824
	Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val	
	595 600 605	
40	AAC CGC ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC	1872
	Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile	
	610 615 620	
45	CTG GGG CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC	1920
	Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile	
	625 630 635 640	
50	ATG GCC GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC	1968
	Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg	
	645 650 655	
55	CAC AAC ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG	2016
	His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln	
	660 665 670	
60	AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC	2064
	Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr	
	675 680 685	
65	CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT	2112
	Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp	
	690 695 700	
70	CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC	2160
	His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly	
	705 710 715 720	

157

158

ATG GAC GAG CTG TAC AAG TAA  
Met Asp Glu Leu Tyr Lys  
725

2181

5

## (2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 726 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- 15 (ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

20 Met Ser Asp Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly  
1 5 10 15  
Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp  
20 25 30  
Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg  
25 35 40 45  
Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys  
50 55 60  
Thr Glu Arg Pro Arg Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp  
65 70 75 80  
30 Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg  
85 90 95  
Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala Asp Gly Leu Lys Lys  
100 105 110  
Gln Glu Glu Glu Glu Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn  
35 115 120 125  
Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys His Arg  
130 135 140  
Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr  
145 150 155 160  
40 Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr  
165 170 175  
Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val  
180 185 190  
Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro  
45 195 200 205  
Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys  
210 215 220  
Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser  
225 230 235 240  
50 Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu  
245 250 255  
Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr  
260 265 270  
Arg Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile  
55 275 280 285  
Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala

158

159

		Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val
	5	305					310					315					320
		Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly
						325					330						335
		Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	Gln
					340					345					350		
		Asp	His	Glu	Lys	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Glu	Ile	Arg	Phe
				355					360					365			
10		Pro	Arg	Thr	Leu	Gly	Pro	Glu	Ala	Lys	Ser	Leu	Leu	Ser	Gly	Leu	Leu
			370					375					380				
		Lys	Lys	Asp	Pro	Lys	Gln	Arg	Leu	Gly	Gly	Gly	Ser	Glu	Asp	Ala	Lys
		385					390					395					400
		Glu	Ile	Met	Gln	His	Arg	Phe	Phe	Ala	Gly	Ile	Val	Trp	Gln	His	Val
15						405					410					415	
		Tyr	Glu	Lys	Lys	Leu	Ser	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser	Glu
					420					425					430		
		Thr	Asp	Thr	Arg	Tyr	Phe	Asp	Glu	Glu	Phe	Thr	Ala	Gln	Met	Ile	Thr
				435					440					445			
20		Ile	Thr	Pro	Pro	Asp	Gln	Asp	Asp	Ser	Met	Glu	Cys	Val	Asp	Ser	Glu
			450					455					460				
		Arg	Arg	Pro	His	Phe	Pro	Gln	Phe	Ser	Tyr	Ser	Ala	Ser	Ser	Thr	Ala
		465					470					475					480
		Ser	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe
25						485					490					495	
		Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly
					500					505					510		
		His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly
				515					520					525			
30		Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro
			530					535					540				
		Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser
		545					550					555					560
		Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met
35						565					570					575	
		Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly
					580					585					590		
		Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val
				595					600					605			
40		Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile
			610					615					620				
		Leu	Gly														

160

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2751 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## 10 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...2748  
 (D) OTHER INFORMATION:

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

20	ATG GCT GAC GTT TAC CCG GCC AAC GAC TCC ACG GCG TCT CAG GAC GTG	48
	Met Ala Asp Val Tyr Pro Ala Asn Asp Ser Thr Ala Ser Gln Asp Val	
	1 5 10 15	
	GCC AAC CGC TTC GCC CGC AAA GGG GCG CTG AGG CAG AAG AAC GTG CAT	96
	Ala Asn Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn Val His	
	20 25 30	
25	GAG GTG AAA GAC CAC AAA TTC ATC GCC CGC TTC TTC AAG CAA CCC ACC	144
	Glu Val Lys Asp His Lys Phe Ile Ala Arg Phe Phe Lys Gln Pro Thr	
	35 40 45	
30	TTC TGC AGC CAC TGC ACC GAC TTC ATC TGG GGG TTT GGG AAA CAA GGC	192
	Phe Cys Ser His Cys Thr Asp Phe Ile Trp Gly Phe Gly Lys Gln Gly	
	50 55 60	
35	TTC CAG TGC CAA GTT TGC TGT TTT GTG GTT CAT AAG AGG TGC CAT GAG	240
	Phe Gln Cys Gln Val Cys Cys Phe Val Val His Lys Arg Cys His Glu	
	65 70 75 80	
40	TTC GTT ACG TTC TCT TGT CCG GGT GCG GAT AAG GGA CCT GAC ACT GAC	288
	Phe Val Thr Phe Ser Cys Pro Gly Ala Asp Lys Gly Pro Asp Thr Asp	
	85 90 95	
	GAC CCC AGG AGC AAG CAC AAG TTC AAA ATC CAC ACA TAC GGA AGC CCT	336
	Asp Pro Arg Ser Lys His Lys Phe Lys Ile His Thr Tyr Gly Ser Pro	
	100 105 110	
45	ACC TTC TGT GAT CAC TGT GGG TCC CTG CTC TAT GGA CTT ATC CAC CAA	384
	Thr Phe Cys Asp His Cys Gly Ser Leu Leu Tyr Gly Leu Ile His Gln	
	115 120 125	
50	GGG ATG AAA TGT GAC ACC TGC GAC ATG AAT GTT CAC AAC CAG TGT GTG	432
	Gly Met Lys Cys Asp Thr Cys Asp Met Asn Val His Asn Gln Cys Val	
	130 135 140	
55	ATC AAT GAC CCT AGC CTC TGC GGA ATG GAT CAC ACA GAG AAG AGG GGG	480
	Ile Asn Asp Pro Ser Leu Cys Gly Met Asp His Thr Glu Lys Arg Gly	
	145 150 155 160	

160

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	CGG	ATT	TAT	CTG	AAG	GCT	GAG	GTC	ACT	GAT	GAA	AAG	CTC	CAC	GTC	ACG	528
	Arg	Ile	Tyr	Leu	Lys	Ala	Glu	Val	Thr	Asp	Glu	Lys	Leu	His	Val	Thr	
					165					170					175		
5	GTA	CGA	GAT	GCA	AAA	AAT	CTA	ATC	CCT	ATG	GAT	CCA	AAT	GGG	CTT	TCG	576
	Val	Arg	Asp	Ala	Lys	Asn	Leu	Ile	Pro	Met	Asp	Pro	Asn	Gly	Leu	Ser	
				180					185					190			
10	GAT	CCT	TAT	GTG	AAG	CTG	AAA	CTA	ATC	CCT	GAC	CCC	AAG	AAT	GAG	AGC	624
	Asp	Pro	Tyr	Val	Lys	Leu	Lys	Leu	Ile	Pro	Asp	Pro	Lys	Asn	Glu	Ser	
			195					200					205				
15	AAA	CAG	AAA	ACC	AAA	ACC	ATC	CGC	TCC	AAC	CTG	AAT	CCT	CAG	TGG	AAT	672
	Lys	Gln	Lys	Thr	Lys	Thr	Ile	Arg	Ser	Asn	Leu	Asn	Pro	Gln	Trp	Asn	
		210					215					220					
20	GAG	TCC	TTC	ACG	TTC	AAA	TTA	AAA	CCT	TCA	GAC	AAA	GAC	CGG	CGA	CTG	720
	Glu	Ser	Phe	Thr	Phe	Lys	Leu	Lys	Pro	Ser	Asp	Lys	Asp	Arg	Arg	Leu	
	225					230				235					240		
25	TCT	GTA	GAA	ATC	TGG	GAC	TGG	GAT	CGG	ACG	ACT	CGG	AAT	GAC	TTC	ATG	768
	Ser	Val	Glu	Ile	Trp	Asp	Trp	Asp	Arg	Thr	Thr	Arg	Asn	Asp	Phe	Met	
				245					250						255		
30	GGA	TCC	CTT	TCC	TTT	GGT	GTC	TCA	GAG	CTA	ATG	AAG	ATG	CCG	GCC	AGT	816
	Gly	Ser	Leu	Ser	Phe	Gly	Val	Ser	Glu	Leu	Met	Lys	Met	Pro	Ala	Ser	
				260				265						270			
35	GGA	TGG	TAT	AAA	GCT	CAC	AAC	CAA	GAA	GAG	GGC	GAA	TAT	TAC	AAC	GTG	864
	Gly	Trp	Tyr	Lys	Ala	His	Asn	Gln	Glu	Glu	Gly	Glu	Tyr	Tyr	Asn	Val	
		275					280						285				
40	CCC	ATT	CCA	GAA	GGA	GAT	GAA	GAA	GGC	AAC	ATG	GAA	CTC	AGG	CAG	AAG	912
	Pro	Ile	Pro	Glu	Gly	Asp	Glu	Glu	Gly	Asn	Met	Glu	Leu	Arg	Gln	Lys	
		290				295						300					
45	TTT	GAG	AAA	GCC	AAG	CTA	GGT	CCT	GTT	GGT	AAC	AAA	GTC	ATC	AGC	CCT	960
	Phe	Glu	Lys	Ala	Lys	Leu	Gly	Pro	Val	Gly	Asn	Lys	Val	Ile	Ser	Pro	
	305					310				315					320		
50	TCA	GAA	GAC	AGA	AAG	CAA	CCA	TCC	AAC	AAC	CTG	GAC	AGA	GTG	AAA	CTC	1008
	Ser	Glu	Asp	Arg	Lys	Gln	Pro	Ser	Asn	Asn	Leu	Asp	Arg	Val	Lys	Leu	
				325					330					335			
55	ACA	GAC	TTC	AAC	TTC	CTC	ATG	GTG	CTG	GGG	AAG	GGG	AGT	TTT	GGG	AAG	1056
	Thr	Asp	Phe	Asn	Phe	Leu	Met	Val	Leu	Gly	Lys	Gly	Ser	Phe	Gly	Lys	
				340					345					350			
60	GTG	ATG	CTT	GCT	GAC	AGG	AAG	GGA	ACG	GAG	GAA	CTG	TAC	GCC	ATC	AAG	1104
	Val	Met	Leu	Ala	Asp	Arg	Lys	Gly	Thr	Glu	Glu	Leu	Tyr	Ala	Ile	Lys	
			355					360					365				
65	ATC	CTG	AAG	AAG	GAC	GTG	GTG	ATC	CAG	GAC	GAC	GAC	GTG	GAG	TGC	ACC	1152
	Ile	Leu	Lys	Lys	Asp	Val	Val	Ile	Gln	Asp	Asp	Asp	Val	Glu	Cys	Thr	
		370					375					380					

161

	ATG GTG GAG AAG CGC GTG CTG GCC CTG CTG GAC AAG CCG CCA TTT CTG	1200
	Met Val Glu Lys Arg Val Leu Ala Leu Leu Asp Lys Pro Pro Phe Leu	400
	385 390 395	
5	ACA CAG CTG CAC TCC TGC TTC CAG ACA GTG GAC CGG CTG TAC TTC GTC	1248
	Thr Gln Leu His Ser Cys Phe Gln Thr Val Asp Arg Leu Tyr Phe Val	415
	405 410	
10	ATG GAA TAC GTC AAC GGC GGG GAT CTT ATG TAC CAC ATT CAG CAA GTC	1296
	Met Glu Tyr Val Asn Gly Gly Asp Leu Met Tyr His Ile Gln Gln Val	430
	420 425	
15	GGG AAA TTT AAG GAG CCA CAA GCA GTA TTC TAC GCA GCC GAG ATC TCC	1344
	Gly Lys Phe Lys Glu Pro Gln Ala Val Phe Tyr Ala Ala Glu Ile Ser	445
	435 440	
20	ATC GGA CTG TTC TTC CTT CAT AAA AGA GGG ATC ATT TAC AGG GAT CTG	1392
	Ile Gly Leu Phe Phe Leu His Lys Arg Gly Ile Ile Tyr Arg Asp Leu	460
	450 455	
	AAG CTG AAC AAT GTC ATG CTG AAC TCA GAA GGG CAC ATC AAA ATC GCC	1440
	Lys Leu Asn Asn Val Met Leu Asn Ser Glu Gly His Ile Lys Ile Ala	480
	465 470 475	
25	GAC TTC GGG ATG TGC AAG GAA CAC ATG ATG GAT GGA GTC ACG ACC AGG	1488
	Asp Phe Gly Met Cys Lys Glu His Met Met Asp Gly Val Thr Thr Arg	495
	485 490	
30	ACC TTC TGC GGA ACT CCG GAC TAC ATT GCC CCA GAG ATA ATC GCT TAC	1536
	Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr	510
	500 505	
35	CAG CCG TAC GGG AAG TCT GTA GAT TGG TGG GCG TAC GGT GTG CTG CTG	1584
	Gln Pro Tyr Gly Lys Ser Val Asp Trp Trp Ala Tyr Gly Val Leu Leu	525
	515 520	
40	TAC GAG ATG CTA GCC GGG CAG CCT CCG TTT GAT GGT GAA GAT GAA GAT	1632
	Tyr Glu Met Leu Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Asp	540
	530 535	
45	GAA CTG TTT CAG TCT ATA ATG GAG CAC AAC GTG TCC TAC CCC AAA TCC	1680
	Glu Leu Phe Gln Ser Ile Met Glu His Asn Val Ser Tyr Pro Lys Ser	560
	545 550 555	
	TTG TCC AAG GAA GCC GTC TCC ATC TGC AAA GGA CTT ATG ACC AAA CAG	1728
	Leu Ser Lys Glu Ala Val Ser Ile Cys Lys Gly Leu Met Thr Lys Gln	575
	565 570	
50	CCT GCC AAG CGA CTG GGC TGC GGG CCC GAG GGA GAG AGG GAT GTC AGA	1776
	Pro Ala Lys Arg Leu Gly Cys Gly Pro Glu Gly Glu Arg Asp Val Arg	590
	580 585	
55	GAG CAT GCC TTC TTC AGG AGG ATC GAC TGG GAG AAA CTG GAG AAC AGG	1824
	Glu His Ala Phe Phe Arg Arg Ile Asp Trp Glu Lys Leu Glu Asn Arg	605
	595 600	

163

	GAG ATC CAA CCA CCA TTC AAG CCC AAA GTG TGT GGC AAA GGA GCA GAA	1872
	Glu Ile Gln Pro Pro Phe Lys Pro Lys Val Cys Gly Lys Gly Ala Glu	
	610 615 620	
5	AAC TTT GAC AAG TTC TTC ACG CGA GGA CAG CCT GTC TTA ACA CCA CCA	1920
	Asn Phe Asp Lys Phe Phe Thr Arg Gly Gln Pro Val Leu Thr Pro Pro	
	625 630 635 640	
10	GAT CAG CTG GTC ATT GCT AAC ATA GAC CAA TCT GAT TTT GAA GGG TTC	1968
	Asp Gln Leu Val Ile Ala Asn Ile Asp Gln Ser Asp Phe Glu Gly Phe	
	645 650 655	
15	TCG TAT GTC AAC CCC CAG TTT GTG CAC CCA ATC TTG CAA AGT GCA GTA	2016
	Ser Tyr Val Asn Pro Gln Phe Val His Pro Ile Leu Gln Ser Ala Val	
	660 665 670	
20	GGG CGC GCC ATG AGT AAA GGA GAA GAA CTT TTC ACT GGA GTT GTC CCA	2064
	Gly Arg Ala Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro	
	675 680 685	
25	ATT CTT GTT GAA TTA GAT GGC GAT GTT AAT GGG CAA AAA TTC TCT GTT	2112
	Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val	
	690 695 700	
30	AGT GGA GAG GGT GAA GGT GAT GCA ACA TAC GGA AAA CTT ACC CTT AAA	2160
	Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys	
	705 710 715 720	
35	TTT ATT TGC ACT ACT GGG AAG CTA CCT GTT CCA TGG CCA ACG CTT GTC	2208
	Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val	
	725 730 735	
40	ACT ACT CTC ACT TAT GGT GTT CAA TGC TTT TCT AGA TAC CCA GAT CAT	2256
	Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His	
	740 745 750	
45	ATG AAA CAG CAT GAC TTT TTC AAG AGT GCC ATG CCC GAA GGT TAT GTA	2304
	Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val	
	755 760 765	
50	CAG GAA AGA ACT ATA TTT TAC AAA GAT GAC GGG AAC TAC AAG ACA CGT	2352
	Gln Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg	
	770 775 780	
55	GCT GAA GTC AAG TTT GAA GGT GAT ACC CTT GTT AAT AGA ATC GAG TTA	2400
	Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu	
	785 790 795 800	
60	AAA GGT ATT GAT TTT AAA GAA GAT GGA AAC ATT CTT GGA CAC AAA ATG	2448
	Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met	
	805 810 815	
65	GAA TAC AAT TAT AAC TCA CAT AAT GTA TAC ATC ATG GCA GAC AAA CCA	2496
	Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro	
	820 825 830	

163

164

AAG AAT GGC ATC AAA GTT AAC TTC AAA ATT AGA CAC AAC ATT AAA GAT 2544  
 Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp  
                   835                  840                  845

5

GGA AGC GTT CAA TTA GCA GAC CAT TAT CAA CAA AAT ACT CCA ATT GGC 2592  
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly  
                   850                  855                  860

10

GAT GGC CCT GTC CTT TTA CCA GAC AAC CAT TAC CTG TCC ACG CAA TCT 2640  
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser  
                   865                  870                  875                  880

15

GCC CTT TCC AAA GAT CCC AAC GAA AAG AGA GAT CAC ATG ATC CTT CTT 2688  
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu  
                   885                  890                  895

20

GAG TTT GTA ACA GCT GCT GGG ATT ACA CAT GGC ATG GAT GAA CTA TAC 2736  
 Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr  
                   900                  905                  910

AAA CCT CAG GAG TAA 2751  
 Lys Pro Gln Glu  
                   915

25

## (2) INFORMATION FOR SEQ ID NO:73:

## (i) SEQUENCE CHARACTERISTICS:

- 30
- (A) LENGTH: 916 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

- 35
- (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

40 Met Ala Asp Val Tyr Pro Ala Asn Asp Ser Thr Ala Ser Gln Asp Val  
     1                  5                  10                  15  
 Ala Asn Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn Val His  
                   20                  25                  30  
 Glu Val Lys Asp His Lys Phe Ile Ala Arg Phe Phe Lys Gln Pro Thr  
 45                   35                  40                  45  
 Phe Cys Ser His Cys Thr Asp Phe Ile Trp Gly Phe Gly Lys Gln Gly  
                   50                  55                  60  
 Phe Gln Cys Gln Val Cys Cys Phe Val Val His Lys Arg Cys His Glu  
                   65                  70                  75                  80  
 50 Phe Val Thr Phe Ser Cys Pro Gly Ala Asp Lys Gly Pro Asp Thr Asp  
                   85                  90                  95  
 Asp Pro Arg Ser Lys His Lys Phe Lys Ile His Thr Tyr Gly Ser Pro  
                   100                  105                  110  
 Thr Phe Cys Asp His Cys Gly Ser Leu Leu Tyr Gly Leu Ile His Gln  
 55                   115                  120                  125  
 Gly Met Lys Cys Asp Thr Cys Asp Met Asn Val His Asn Gln Cys Val

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	130		135		140														
	Ile	Asn	Asp	Pro	Ser	Leu	Cys	Gly	Met	Asp	His	Thr	Glu	Lys	Arg	Gly			
	145					150					155					160			
	Arg	Ile	Tyr	Leu	Lys	Ala	Glu	Val	Thr	Asp	Glu	Lys	Leu	His	Val	Thr			
5					165					170					175				
	Val	Arg	Asp	Ala	Lys	Asn	Leu	Ile	Pro	Met	Asp	Pro	Asn	Gly	Leu	Ser			
				180					185					190					
	Asp	Pro	Tyr	Val	Lys	Leu	Lys	Leu	Ile	Pro	Asp	Pro	Lys	Asn	Glu	Ser			
			195					200					205						
10	Lys	Gln	Lys	Thr	Lys	Thr	Ile	Arg	Ser	Asn	Leu	Asn	Pro	Gln	Trp	Asn			
	210					215						220							
	Glu	Ser	Phe	Thr	Phe	Lys	Leu	Lys	Pro	Ser	Asp	Lys	Asp	Arg	Arg	Leu			
	225					230					235					240			
	Ser	Val	Glu	Ile	Trp	Asp	Trp	Asp	Arg	Thr	Thr	Arg	Asn	Asp	Phe	Met			
15					245					250					255				
	Gly	Ser	Leu	Ser	Phe	Gly	Val	Ser	Glu	Leu	Met	Lys	Met	Pro	Ala	Ser			
				260					265					270					
	Gly	Trp	Tyr	Lys	Ala	His	Asn	Gln	Glu	Glu	Gly	Glu	Tyr	Tyr	Asn	Val			
			275				280					285							
20	Pro	Ile	Pro	Glu	Gly	Asp	Glu	Gly	Asn	Met	Glu	Leu	Arg	Gln	Lys				
	290					295					300								
	Phe	Glu	Lys	Ala	Lys	Leu	Gly	Pro	Val	Gly	Asn	Lys	Val	Ile	Ser	Pro			
	305					310					315				320				
	Ser	Glu	Asp	Arg	Lys	Gln	Pro	Ser	Asn	Asn	Leu	Asp	Arg	Val	Lys	Leu			
25					325					330					335				
	Thr	Asp	Phe	Asn	Phe	Leu	Met	Val	Leu	Gly	Lys	Gly	Ser	Phe	Gly	Lys			
				340					345					350					
	Val	Met	Leu	Ala	Asp	Arg	Lys	Gly	Thr	Glu	Glu	Leu	Tyr	Ala	Ile	Lys			
			355				360					365							
30	Ile	Leu	Lys	Lys	Asp	Val	Val	Ile	Gln	Asp	Asp	Asp	Val	Glu	Cys	Thr			
	370					375					380								
	Met	Val	Glu	Lys	Arg	Val	Leu	Ala	Leu	Leu	Asp	Lys	Pro	Pro	Phe	Leu			
	385					390					395				400				
	Thr	Gln	Leu	His	Ser	Cys	Phe	Gln	Thr	Val	Asp	Arg	Leu	Tyr	Phe	Val			
35					405					410					415				
	Met	Glu	Tyr	Val	Asn	Gly	Gly	Asp	Leu	Met	Tyr	His	Ile	Gln	Gln	Val			
				420				425						430					
	Gly	Lys	Phe	Lys	Glu	Pro	Gln	Ala	Val	Phe	Tyr	Ala	Ala	Glu	Ile	Ser			
			435				440					445							
40	Ile	Gly	Leu	Phe	Phe	Leu	His	Lys	Arg	Gly	Ile	Ile	Tyr	Arg	Asp	Leu			
	450					455					460								
	Lys	Leu	Asn	Asn	Val	Met	Leu	Asn	Ser	Glu	Gly	His	Ile	Lys	Ile	Ala			
	465					470					475				480				
	Asp	Phe	Gly	Met	Cys	Lys	Glu	His	Met	Met	Asp	Gly	Val	Thr	Thr	Arg			
45					485					490					495				
	Thr	Phe	Cys	Gly	Thr	Pro	Asp	Tyr	Ile	Ala	Pro	Glu	Ile	Ile	Ala	Tyr			
				500				505						510					
	Gln	Pro	Tyr	Gly	Lys	Ser	Val	Asp	Trp	Trp	Ala	Tyr	Gly	Val	Leu	Leu			
			515				520					525							
50	Tyr	Glu	Met	Leu	Ala	Gly	Gln	Pro	Pro	Phe	Asp	Gly	Glu	Asp	Glu	Asp			
	530					535					540								
	Glu	Leu	Phe	Gln	Ser	Ile	Met	Glu	His	Asn	Val	Ser	Tyr	Pro	Lys	Ser			
	545					550					555				560				
	Leu	Ser	Lys	Glu	Ala	Val	Ser	Ile	Cys	Lys	Gly	Leu	Met	Thr	Lys	Gln			
55					565					570					575				
	Pro	Ala	Lys	Arg	Leu	Gly	Cys	Gly	Pro	Glu	Gly	Glu	Arg	Asp	Val	Arg			

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			580				585				590			
			Glu His Ala Phe Phe Arg Arg Ile Asp Trp Glu Lys Leu Glu Asn Arg											
			595				600				605			
			Glu Ile Gln Pro Pro Phe Lys Pro Lys Val Cys Gly Lys Gly Ala Glu											
5			610				615				620			
			Asn Phe Asp Lys Phe Phe Thr Arg Gly Gln Pro Val Leu Thr Pro Pro											
			625				630				635			640
			Asp Gln Leu Val Ile Ala Asn Ile Asp Gln Ser Asp Phe Glu Gly Phe											
							645				650			655
10			Ser Tyr Val Asn Pro Gln Phe Val His Pro Ile Leu Gln Ser Ala Val											
			660				665				670			
			Gly Arg Ala Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro											
			675				680				685			
			Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val											
15			690				695				700			
			Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys											
			705				710				715			720
			Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val											
							725				730			735
20			Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His											
			740				745				750			
			Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val											
			755				760				765			
			Gln Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg											
25			770				775				780			
			Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu											
			785				790				795			800
			Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met											
							805				810			815
30			Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro											
			820				825				830			
			Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp											
			835				840				845			
			Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly											
35			850				855				860			
			Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser											
			865				870				875			880
			Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu											
							885				890			895
40			Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr											
			900				905				910			
			Lys Pro Gln Glu											
			915											

45 (2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2157 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

55

(A) NAME/KEY: Coding Sequence

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(B) LOCATION: 1...2154

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

5	ATG TCG TCC ATC TTG CCA TTC ACG CCG CCA GTT GTG AAG AGA CTG CTG	48
	Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu	
	1 5 10 15	
10	GGA TGG AAG AAG TCA GCT GGT GGG TCT GGA GGA GCA GGC GGA GGA GAG	96
	Gly Trp Lys Lys Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu	
	20 25 30	
15	CAG AAT GGG CAG GAA GAA AAG TGG TGT GAG AAA GCA GTG AAA AGT CTG	144
	Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu	
	35 40 45	
20	GTG AAG AAG CTA AAG AAA ACA GGA CGA TTA GAT GAG CTT GAG AAA GCC	192
	Val Lys Lys Leu Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala	
	50 55 60	
25	ATC ACC ACT CAA AAC TGT AAT ACT AAA TGT GTT ACC ATA CCA AGC ACT	240
	Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr	
	65 70 75 80	
30	TGC TCT GAA ATT TGG GGA CTG AGT ACA CCA AAT ACG ATA GAT CAG TGG	288
	Cys Ser Glu Ile Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp	
	85 90 95	
35	GAT ACA ACA GGC CTT TAC AGC TTC TCT GAA CAA ACC AGG TCT CTT GAT	336
	Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp	
	100 105 110	
40	GGT CGT CTC CAG GTA TCC CAT CGA AAA GGA TTG CCA CAT GTT ATA TAT	384
	Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr	
	115 120 125	
45	TGC CGA TTA TGG CGC TGG CCT GAT CTT CAC AGT CAT CAT GAA CTC AAG	432
	Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys	
	130 135 140	
50	GCA ATT GAA AAC TGC GAA TAT GCT TTT AAT CTT AAA AAG GAT GAA GTA	480
	Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val	
	145 150 155 160	
55	TGT GTA AAC CCT TAC CAC TAT CAG AGA GTT GAG ACA CCA GTT TTG CCT	528
	Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro	
	165 170 175	
60	CCA GTA TTA GTG CCC CGA CAC ACC GAG ATC CTA ACA GAA CTT CCG CCT	576
	Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro	
	180 185 190	
65	CTG GAT GAC TAT ACT CAC TCC ATT CCA GAA AAC ACT AAC TTC CCA GCA	624
	Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala	
	195 200 205	

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5	GGA ATT GAG CCA CAG AGT AAT TAT ATT CCA GAA ACG CCA CCT CCT GGA	672
	Gly Ile Glu Pro Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly	
	210 215 220	
	TAT ATC AGT GAA GAT GGA GAA ACA AGT GAC CAA CAG TTG AAT CAA AGT	720
	Tyr Ile Ser Glu Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser	
10	225 230 235 240	
	ATG GAC ACA GGC TCT CCA GCA GAA CTA TCT CCT ACT ACT CTT TCC CCT	768
	Met Asp Thr Gly Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro	
	245 250 255	
	GTT AAT CAT AGC TTG GAT TTA CAG CCA GTT ACT TAC TCA GAA CCT GCA	816
15	Val Asn His Ser Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala	
	260 265 270	
	TTT TGG TGT TCA ATA GCA TAT TAT GAA TTA AAT CAG AGG GTT GGA GAA	864
	Phe Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu	
	275 280 285	
20	ACC TTC CAT GCA TCA CAG CCC TCA CTC ACT GTA GAT GGC TTT ACA GAC	912
	Thr Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp	
	290 295 300	
	CCA TCA AAT TCA GAG AGG TTC TGC TTA GGT TTA CTC TCC AAT GTT AAC	960
	Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn	
25	305 310 315 320	
	CGA AAT GCC ACG GTA GAA ATG ACA AGA AGG CAT ATA GGA AGA GGA GTG	1008
	Arg Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val	
	325 330 335	
	CGC TTA TAC TAC ATA GGT GGG GAA GTT TTT GCT GAG TGC CTA AGT GAT	1056
30	Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp	
	340 345 350	
	AGT GCA ATC TTT GTG CAG AGC CCC AAT TGT AAT CAG AGA TAT GGC TGG	1104
	Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp	
	355 360 365	
35	CAC CCT GCA ACA GTG TGT AAA ATT CCA CCA GGC TGT AAT CTG AAG ATC	1152
	His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile	
	370 375 380	
	TTC AAC AAC CAG GAA TTT GCT GCT CTT CTG GCT CAG TCT GTT AAT CAG	1200
	Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln	
40	385 390 395 400	
	GGT TTT GAA GCC GTC TAT CAG CTA ACT AGA ATG TGC ACC ATA AGA ATG	1248
	Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met	
	405 410 415	
	AGT TTT GTG AAA GGG TGG GGA GCA GAA TAC CGA AGG CAG ACG GTA ACA	1296
45	Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr	
	420 425 430	
50		
55		

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5	AGT ACT CCT TGC TGG ATT GAA CTT CAT CTG AAT GGA CCT CTA CAG TGG	1344
	Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp	
	435 440 445	
10	TTG GAC AAA GTA TTA ACT CAG ATG GGA TCC CCT TCA GTG CGT TGC TCA	1392
	Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser	
	450 455 460	
15	AGC ATG TCA TGG GTA CCG CGG GCC CGG GAT CCA CCG GTC GCC ACC ATG	1440
	Ser Met Ser Trp Val Pro Arg Ala Arg Asp Pro Pro Val Ala Thr Met	
	465 470 475 480	
20	GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG GTC	1488
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
	485 490 495	
25	GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG	1536
	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
	500 505 510	
30	GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC TGC	1584
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
	515 520 525	
35	ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC CTG	1632
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
	530 535 540	
40	ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG CAG	1680
	Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
	545 550 555 560	
45	CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG CGC	1728
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
	565 570 575	
50	ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG GTG	1776
	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
	580 585 590	
55	AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC ATC	1824
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
	595 600 605	
60	GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC AAC	1872
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
	610 615 620	
65	TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC GGC	1920
	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
	625 630 635 640	
70	ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG	1968
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
	645 650 655	

169

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CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC 2016  
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
 660 665 670  
 5 GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC 2064  
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
 675 680 685  
 10 AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG 2112  
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 690 695 700  
 15 ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA 2157  
 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 705 710 715

## (2) INFORMATION FOR SEQ ID NO:75:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 25 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu  
 1 5 10 15  
 Gly Trp Lys Lys Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu  
 35 20 25 30  
 Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu  
 35 40 45  
 Val Lys Lys Leu Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala  
 50 55 60  
 40 Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr  
 65 70 75 80  
 Cys Ser Glu Ile Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp  
 85 90 95  
 Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp  
 45 100 105 110  
 Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr  
 115 120 125  
 Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys  
 130 135 140  
 50 Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val  
 145 150 155 160  
 Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro  
 165 170 175  
 Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro  
 55 180 185 190  
 Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala

170

171

[illegible]

171

172

645 650 655  
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
 660 665 670  
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
 675 680 685  
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 690 695 700  
 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 705 710 715

10

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 2397 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...2394  
 (D) OTHER INFORMATION:

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATG GAC AAT ATG TCT ATT ACG AAT ACA CCA ACA AGT AAT GAT GCC TGT 48  
 Met Asp Asn Met Ser Ile Thr Asn Thr Pro Thr Ser Asn Asp Ala Cys  
 30 1 5 10 15  
 CTG AGC ATT GTG CAT AGT TTG ATG TGC CAT AGA CAA GGT GGA GAG AGT 96  
 Leu Ser Ile Val His Ser Leu Met Cys His Arg Gln Gly Gly Glu Ser  
 20 25 30  
 GAA ACA TTT GCA AAA AGA GCA ATT GAA AGT TTG GTA AAG AAG CTG AAG 144  
 Glu Thr Phe Ala Lys Arg Ala Ile Glu Ser Leu Val Lys Lys Leu Lys  
 35 40 45  
 GAG AAA AAA GAT GAA TTG GAT TCT TTA ATA ACA GCT ATA ACT ACA AAT 192  
 Glu Lys Lys Asp Glu Leu Asp Ser Leu Ile Thr Ala Ile Thr Thr Asn  
 50 55 60  
 GGA GCT CAT CCT AGT AAA TGT GTT ACC ATA CAG AGA ACA TTG GAT GGG 240  
 Gly Ala His Pro Ser Lys Cys Val Thr Ile Gln Arg Thr Leu Asp Gly  
 65 70 75 80  
 AGG CTT CAG GTG GCT GGT CGG AAA GGA TTT CCT CAT GTG ATC TAT GCC 288  
 Arg Leu Gln Val Ala Gly Arg Lys Gly Phe Pro His Val Ile Tyr Ala  
 85 90 95  
 CGT CTC TGG AGG TGG CCT GAT CTT CAC AAA AAT GAA CTA AAA CAT GTT 336  
 Arg Leu Trp Arg Trp Pro Asp Leu His Lys Asn Glu Leu Lys His Val  
 100 105 110  
 AAA TAT TGT CAG TAT GCG TTT GAC TTA AAA TGT GAT AGT GTC TGT GTG 384

55

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	Lys	Tyr	Cys	Gln	Tyr	Ala	Phe	Asp	Leu	Lys	Cys	Asp	Ser	Val	Cys	Val	
			115					120						125			
5	AAT	CCA	TAT	CAC	TAC	GAA	CGA	GTT	GTA	TCA	CCT	GGA	ATT	GAT	CTC	TCA	432
	Asn	Pro	Tyr	His	Tyr	Glu	Arg	Val	Val	Ser	Pro	Gly	Ile	Asp	Leu	Ser	
			130				135					140					
10	GGA	TTA	ACA	CTG	CAG	AGT	AAT	GCT	CCA	TCA	AGT	ATG	ATG	GTG	AAG	GAT	480
	Gly	Leu	Thr	Leu	Gln	Ser	Asn	Ala	Pro	Ser	Ser	Met	Met	Val	Lys	Asp	
		145				150					155					160	
15	GAA	TAT	GTG	CAT	GAC	TTT	GAG	GGA	CAG	CCA	TCG	TTG	TCC	ACT	GAA	GGA	528
	Glu	Tyr	Val	His	Asp	Phe	Glu	Gly	Gln	Pro	Ser	Leu	Ser	Thr	Glu	Gly	
					165					170					175		
20	CAT	TCA	ATT	CAA	ACC	ATC	CAG	CAT	CCA	CCA	AGT	AAT	CGT	GCA	TCG	ACA	576
	His	Ser	Ile	Gln	Thr	Ile	Gln	His	Pro	Pro	Ser	Asn	Arg	Ala	Ser	Thr	
					180					185					190		
25	GAG	ACA	TAC	AGC	ACC	CCA	GCT	CTG	TTA	GCC	CCA	TCT	GAG	TCT	AAT	GCT	624
	Glu	Thr	Tyr	Ser	Thr	Pro	Ala	Leu	Leu	Ala	Pro	Ser	Glu	Ser	Asn	Ala	
					195			200					205				
30	ACC	AGC	ACT	GCC	AAC	TTT	CCC	AAC	ATT	CCT	GTG	GCT	TCC	ACA	AGT	CAG	672
	Thr	Ser	Thr	Ala	Asn	Phe	Pro	Asn	Ile	Pro	Val	Ala	Ser	Thr	Ser	Gln	
			210					215				220					
35	CCT	GCC	AGT	ATA	CTG	GGG	GGC	AGC	CAT	AGT	GAA	GGA	CTG	TTG	CAG	ATA	720
	Pro	Ala	Ser	Ile	Leu	Gly	Gly	Ser	His	Ser	Glu	Gly	Leu	Leu	Gln	Ile	
					230						235				240		
40	GCA	TCA	GGG	CCT	CAG	CCA	GGA	CAG	CAG	CAG	AAT	GGA	TTT	ACT	GGT	CAG	768
	Ala	Ser	Gly	Pro	Gln	Pro	Gly	Gln	Gln	Gln	Asn	Gly	Phe	Thr	Gly	Gln	
					245					250					255		
45	CCA	GCT	ACT	TAC	CAT	CAT	AAC	AGC	ACT	ACC	ACC	TGG	ACT	GGA	AGT	AGG	816
	Pro	Ala	Thr	Tyr	His	His	Asn	Ser	Thr	Thr	Thr	Trp	Thr	Gly	Ser	Arg	
					260					265				270			
50	ACT	GCA	CCA	TAC	ACA	CCT	AAT	TTG	CCT	CAC	CAC	CAA	AAC	GGC	CAT	CTT	864
	Thr	Ala	Pro	Tyr	Thr	Pro	Asn	Leu	Pro	His	His	Gln	Asn	Gly	His	Leu	
					275			280					285				
55	CAG	CAC	CAC	CCG	CCT	ATG	CCG	CCC	CAT	CCC	GGA	CAT	TAC	TGG	CCT	GTT	912
	Gln	His	His	Pro	Pro	Met	Pro	Pro	His	Pro	Gly	His	Tyr	Trp	Pro	Val	
					290			295				300					
60	CAC	AAT	GAG	CTT	GCA	TTC	CAG	CCT	CCC	ATT	TCC	AAT	CAT	CCT	GCT	CCT	960
	His	Asn	Glu	Leu	Ala	Phe	Gln	Pro	Pro	Ile	Ser	Asn	His	Pro	Ala	Pro	
					305		310				315				320		
65	GAG	TAT	TGG	TGT	TCC	ATT	GCT	TAC	TTT	GAA	ATG	GAT	GTT	CAG	GTA	GGA	1008
	Glu	Tyr	Trp	Cys	Ser	Ile	Ala	Tyr	Phe	Glu	Met	Asp	Val	Gln	Val	Gly	
					325					330					335		
70	GAG	ACA	TTT	AAG	GTT	CCT	TCA	AGC	TGC	CCT	ATT	GTT	ACT	GTT	GAT	GGA	1056

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	Glu Thr Phe Lys Val Pro Ser Ser Cys Pro Ile Val Thr Val Asp Gly	
	340 345 350	
5	TAC GTG GAC CCT TCT GGA GGA GAT CGC TTT TGT TTG GGT CAA CTC TCC Tyr Val Asp Pro Ser Gly Gly Asp Arg Phe Cys Leu Gly Gln Leu Ser	1104
	355 360 365	
10	AAT GTC CAC AGG ACA GAA GCC ATT GAG AGA GCA AGG TTG CAC ATA GGC Asn Val His Arg Thr Glu Ala Ile Glu Arg Ala Arg Leu His Ile Gly	1152
	370 375 380	
15	AAA GGT GTG CAG TTG GAA TGT AAA GGT GAA GGT GAT GTT TGG GTC AGG Lys Gly Val Gln Leu Glu Cys Lys Gly Glu Gly Asp Val Trp Val Arg	1200
	385 390 395 400	
	TGC CTT AGT GAC CAC GCG GTC TTT GTA CAG AGT TAC TAC TTA GAC AGA Cys Leu Ser Asp His Ala Val Phe Val Gln Ser Tyr Tyr Leu Asp Arg	1248
	405 410 415	
20	GAA GCT GGG CGT GCA CCT GGA GAT GCT GTT CAT AAG ATC TAC CCA AGT Glu Ala Gly Arg Ala Pro Gly Asp Ala Val His Lys Ile Tyr Pro Ser	1296
	420 425 430	
25	GCA TAT ATA AAG GTC TTT GAT TTG CGT CAG TGT CAT CGA CAG ATG CAG Ala Tyr Ile Lys Val Phe Asp Leu Arg Gln Cys His Arg Gln Met Gln	1344
	435 440 445	
30	CAG CAG GCG GCT ACT GCA CAA GCT GCA GCA GCT GCC CAG GCA GCA GCC Gln Gln Ala Ala Thr Ala Gln Ala Ala Ala Ala Ala Gln Ala Ala Ala	1392
	450 455 460	
35	GTG GCA GGA AAC ATC CCT GGC CCA GGA TCA GTA GGT GGA ATA GCT CCA Val Ala Gly Asn Ile Pro Gly Pro Gly Ser Val Gly Gly Ile Ala Pro	1440
	465 470 475 480	
	GCT ATC AGT CTG TCA GCT GCT GCT GGA ATT GGT GTT GAT GAC CTT CGT Ala Ile Ser Leu Ser Ala Ala Ala Gly Ile Gly Val Asp Asp Leu Arg	1488
	485 490 495	
40	CGC TTA TGC ATA CTC AGG ATG AGT TTT GTG AAA GGC TGG GGA CCG GAT Arg Leu Cys Ile Leu Arg Met Ser Phe Val Lys Gly Trp Gly Pro Asp	1536
	500 505 510	
45	TAC CCA AGA CAG AGC ATC AAA GAA ACA CCT TGC TGG ATT GAA ATT CAC Tyr Pro Arg Gln Ser Ile Lys Glu Thr Pro Cys Trp Ile Glu Ile His	1584
	515 520 525	
50	TTA CAC CGG GCC CTC CAG CTC CTA GAC GAA GTA CTT CAT ACC ATG CCG Leu His Arg Ala Leu Gln Leu Leu Asp Glu Val Leu His Thr Met Pro	1632
	530 535 540	
55	ATT GCA GAC CCA CAA CCT TTA GAC TGG GAT CCA CCG GTC GCC ACC ATG Ile Ala Asp Pro Gln Pro Leu Asp Trp Asp Pro Pro Val Ala Thr Met	1680
	545 550 555 560	
	GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG GTC	1728

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175																
	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
	565				570				575							
5	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG
	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
	580				585				590							
10	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC
	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
	595				600				605							
15	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG
	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu
	610				615				620							
20	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG
	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln
	625				630				635				640			
25	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC
	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
	645				650				655							
30	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG
	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
	660				665				670							
35	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC
	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
	675				680				685							
40	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC
	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
	690				695				700							
45	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC
	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
	705				710				715				720			
50	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	GTG
	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val
	725				730				735							
55	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	CCC
	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
	740				745				750							
60	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	AGC
	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
	755				760				765							
65	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	GTG
	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
	770				775				780							
70	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TAA	

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Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
785 790 795

5 (2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 amino acids  
(B) TYPE: amino acid  
10 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

	Met	Asp	Asn	Met	Ser	Ile	Thr	Asn	Thr	Pro	Thr	Ser	Asn	Asp	Ala	Cys
	1				5					10					15	
20	Leu	Ser	Ile	Val	His	Ser	Leu	Met	Cys	His	Arg	Gln	Gly	Gly	Glu	Ser
				20					25					30		
	Glu	Thr	Phe	Ala	Lys	Arg	Ala	Ile	Glu	Ser	Leu	Val	Lys	Lys	Leu	Lys
			35				40					45				
	Glu	Lys	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Ile	Thr	Ala	Ile	Thr	Thr	Asn
25		50					55				60					
	Gly	Ala	His	Pro	Ser	Lys	Cys	Val	Thr	Ile	Gln	Arg	Thr	Leu	Asp	Gly
	65					70				75					80	
	Arg	Leu	Gln	Val	Ala	Gly	Arg	Lys	Gly	Phe	Pro	His	Val	Ile	Tyr	Ala
				85					90					95		
30	Arg	Leu	Trp	Arg	Trp	Pro	Asp	Leu	His	Lys	Asn	Glu	Leu	Lys	His	Val
			100					105					110			
	Lys	Tyr	Cys	Gln	Tyr	Ala	Phe	Asp	Leu	Lys	Cys	Asp	Ser	Val	Cys	Val
			115				120					125				
	Asn	Pro	Tyr	His	Tyr	Glu	Arg	Val	Val	Ser	Pro	Gly	Ile	Asp	Leu	Ser
35		130					135					140				
	Gly	Leu	Thr	Leu	Gln	Ser	Asn	Ala	Pro	Ser	Ser	Met	Met	Val	Lys	Asp
	145					150					155				160	
	Glu	Tyr	Val	His	Asp	Phe	Glu	Gly	Gln	Pro	Ser	Leu	Ser	Thr	Glu	Gly
				165					170					175		
40	His	Ser	Ile	Gln	Thr	Ile	Gln	His	Pro	Pro	Ser	Asn	Arg	Ala	Ser	Thr
			180					185					190			
	Glu	Thr	Tyr	Ser	Thr	Pro	Ala	Leu	Leu	Ala	Pro	Ser	Glu	Ser	Asn	Ala
			195				200					205				
	Thr	Ser	Thr	Ala	Asn	Phe	Pro	Asn	Ile	Pro	Val	Ala	Ser	Thr	Ser	Gln
45		210					215					220				
	Pro	Ala	Ser	Ile	Leu	Gly	Gly	Ser	His	Ser	Glu	Gly	Leu	Leu	Gln	Ile
	225					230					235				240	
	Ala	Ser	Gly	Pro	Gln	Pro	Gly	Gln	Gln	Gln	Asn	Gly	Phe	Thr	Gly	Gln
				245					250					255		
50	Pro	Ala	Thr	Tyr	His	His	Asn	Ser	Thr	Thr	Thr	Trp	Thr	Gly	Ser	Arg
			260					265						270		
	Thr	Ala	Pro	Tyr	Thr	Pro	Asn	Leu	Pro	His	His	Gln	Asn	Gly	His	Leu
		275					280					285				
	Gln	His	His	Pro	Pro	Met	Pro	Pro	His	Pro	Gly	His	Tyr	Trp	Pro	Val
55		290					295				300					
	His	Asn	Glu	Leu	Ala	Phe	Gln	Pro	Pro	Ile	Ser	Asn	His	Pro	Ala	Pro

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	305		310		315		320
	Glu Tyr Trp Cys Ser Ile Ala Tyr Phe Glu Met Asp Val Gln Val Gly						
		325			330		335
5	Glu Thr Phe Lys Val Pro Ser Ser Cys Pro Ile Val Thr Val Asp Gly						
		340			345		350
	Tyr Val Asp Pro Ser Gly Gly Asp Arg Phe Cys Leu Gly Gln Leu Ser						
		355			360		365
	Asn Val His Arg Thr Glu Ala Ile Glu Arg Ala Arg Leu His Ile Gly						
		370			375		380
10	Lys Gly Val Gln Leu Glu Cys Lys Gly Glu Gly Asp Val Trp Val Arg						
		385			390		395
	Cys Leu Ser Asp His Ala Val Phe Val Gln Ser Tyr Tyr Leu Asp Arg						
		405			410		415
15	Glu Ala Gly Arg Ala Pro Gly Asp Ala Val His Lys Ile Tyr Pro Ser						
		420			425		430
	Ala Tyr Ile Lys Val Phe Asp Leu Arg Gln Cys His Arg Gln Met Gln						
		435			440		445
	Gln Gln Ala Ala Thr Ala Gln Ala Ala Ala Ala Gln Ala Ala Ala						
		450			455		460
20	Val Ala Gly Asn Ile Pro Gly Pro Gly Ser Val Gly Gly Ile Ala Pro						
		465			470		475
	Ala Ile Ser Leu Ser Ala Ala Ala Gly Ile Gly Val Asp Asp Leu Arg						
		485			490		495
25	Arg Leu Cys Ile Leu Arg Met Ser Phe Val Lys Gly Trp Gly Pro Asp						
		500			505		510
	Tyr Pro Arg Gln Ser Ile Lys Glu Thr Pro Cys Trp Ile Glu Ile His						
		515			520		525
	Leu His Arg Ala Leu Gln Leu Asp Glu Val Leu His Thr Met Pro						
		530			535		540
30	Ile Ala Asp Pro Gln Pro Leu Asp Trp Asp Pro Pro Val Ala Thr Met						
		545			550		555
	Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val						
		565			570		575
35	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu						
		580			585		590
	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys						
		595			600		605
	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu						
		610			615		620
40	Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln						
		625			630		635
	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg						
		645			650		655
45	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val						
		660			665		670
	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile						
		675			680		685
	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn						
		690			695		700
50	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly						
		705			710		715
	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val						
		725			730		735
	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro						
		740			745		750
55	Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser						

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755                      760                      765  
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 770                      775                      780  
 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 5      785                      790                      795

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- 10      (A) LENGTH: 3138 base pairs  
         (B) TYPE: nucleic acid  
         (C) STRANDEDNESS: single  
         (D) TOPOLOGY: linear

## 15      (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- 20      (A) NAME/KEY: Coding Sequence  
         (B) LOCATION: 1...3135  
         (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

25	ATG GCG GGC TGG ATC CAG GCC CAG CAG CTG CAG GGA GAC GCG CTG CGC	48
	Met Ala Gly Trp Ile Gln Ala Gln Gln Leu Gln Gly Asp Ala Leu Arg	
	1                                      5                                      10                                      15	
30	CAG ATG CAG GTG CTG TAC GGC CAG CAC TTC CCC ATC GAG GTC CGG CAC	96
	Gln Met Gln Val Leu Tyr Gly Gln His Phe Pro Ile Glu Val Arg His	
	20                                      25                                      30	
35	TAC TTG GCC CAG TGG ATT GAG AGC CAG CCA TGG GAT GCC ATT GAC TTG	144
	Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp Asp Ala Ile Asp Leu	
	35                                      40                                      45	
40	GAC AAT CCC CAG GAC AGA GCC CAA GCC ACC CAG CTC CTG GAG GGC CTG	192
	Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln Leu Leu Glu Gly Leu	
	50                                      55                                      60	
45	GTG CAG GAG CTG CAG AAG AAG GCG GAG CAC CAG GTG GGG GAA GAT GGG	240
	Val Gln Glu Leu Gln Lys Lys Ala Glu His Gln Val Gly Glu Asp Gly	
	65                                      70                                      75                                      80	
50	TTT TTA CTG AAG ATC AAG CTG GGG CAC TAC GCC ACG CAG CTC CAG AAA	288
	Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala Thr Gln Leu Gln Lys	
	85                                      90                                      95	
55	ACA TAT GAC CGC TGC CCC CTG GAG CTG GTC CGC TGC ATC CGG CAC ATT	336
	Thr Tyr Asp Arg Cys Pro Leu Glu Leu Val Arg Cys Ile Arg His Ile	
	100                                      105                                      110	
60	CTG TAC AAT GAA CAG AGG CTG GTC CGA GAA GCC AAC AAT TGC AGC TCT	384
	Leu Tyr Asn Glu Gln Arg Leu Val Arg Glu Ala Asn Asn Cys Ser Ser	
	115                                      120                                      125	
65	CCG GCT GGG ATC CTG GTT GAC GCC ATG TCC CAG AAG CAC CTT CAG ATC	432

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	Pro	Ala	Gly	Ile	Leu	Val	Asp	Ala	Met	Ser	Gln	Lys	His	Leu	Gln	Ile	
	130						135					140					
5	AAC	CAG	ACA	TTT	GAG	GAG	CTG	CGA	CTG	GTC	ACG	CAG	GAC	ACA	GAG	AAT	480
	Asn	Gln	Thr	Phe	Glu	Glu	Leu	Arg	Leu	Val	Thr	Gln	Asp	Thr	Glu	Asn	
	145					150					155					160	
10	GAG	CTG	AAG	AAA	CTG	CAG	CAG	ACT	CAG	GAG	TAC	TTC	ATC	ATC	CAG	TAC	528
	Glu	Leu	Lys	Lys	Leu	Gln	Gln	Thr	Gln	Glu	Tyr	Phe	Ile	Ile	Gln	Tyr	
					165					170						175	
15	CAG	GAG	AGC	CTG	AGG	ATC	CAA	GCT	CAG	TTT	GCC	CAG	CTG	GCC	CAG	CTG	576
	Gln	Glu	Ser	Leu	Arg	Ile	Gln	Ala	Gln	Phe	Ala	Gln	Leu	Ala	Gln	Leu	
					180				185						190		
20	AGC	CCC	CAG	GAG	CGT	CTG	AGC	CGG	GAG	ACG	GCC	CTC	CAG	CAG	AAG	CAG	624
	Ser	Pro	Gln	Glu	Arg	Leu	Ser	Arg	Glu	Thr	Ala	Leu	Gln	Gln	Lys	Gln	
			195					200					205				
25	GTG	TCT	CTG	GAG	GCC	TGG	TTG	CAG	CGT	GAG	GCA	CAG	ACA	CTG	CAG	CAG	672
	Val	Ser	Leu	Glu	Ala	Trp	Leu	Gln	Arg	Glu	Ala	Gln	Thr	Leu	Gln	Gln	
		210					215					220					
30	TAC	CGC	GTG	GAG	CTG	GCC	GAG	AAG	CAC	CAG	AAG	ACC	CTG	CAG	CTG	CTG	720
	Tyr	Arg	Val	Glu	Leu	Ala	Glu	Lys	His	Gln	Lys	Thr	Leu	Gln	Leu	Leu	
	225					230					235					240	
35	CGG	AAG	CAG	CAG	ACC	ATC	ATC	CTG	GAT	GAC	GAG	CTG	ATC	CAG	TGG	AAG	768
	Arg	Lys	Gln	Gln	Thr	Ile	Ile	Leu	Asp	Asp	Glu	Leu	Ile	Gln	Trp	Lys	
					245					250					255		
40	CGG	CGG	CAG	CAG	CTG	GCC	GGG	AAC	GGC	GGG	CCC	CCC	GAG	GGC	AGC	CTG	816
	Arg	Arg	Gln	Gln	Leu	Ala	Gly	Asn	Gly	Gly	Pro	Pro	Glu	Gly	Ser	Leu	
					260				265					270			
45	GAC	GTG	CTA	CAG	TCC	TGG	TGT	GAG	AAG	TTG	GCC	GAG	ATC	ATC	TGG	CAG	864
	Asp	Val	Leu	Gln	Ser	Trp	Cys	Glu	Lys	Leu	Ala	Glu	Ile	Ile	Trp	Gln	
		275					280					285					
50	AAC	CGG	CAG	CAG	ATC	CGC	AGG	GCT	GAG	CAC	CTC	TGC	CAG	CAG	CTG	CCC	912
	Asn	Arg	Gln	Gln	Ile	Arg	Arg	Ala	Glu	His	Leu	Cys	Gln	Gln	Leu	Pro	
		290					295					300					
55	ATC	CCC	GGC	CCA	GTG	GAG	GAG	ATG	CTG	GCC	GAG	GTC	AAC	GCC	ACC	ATC	960
	Ile	Pro	Gly	Pro	Val	Glu	Glu	Met	Leu	Ala	Glu	Val	Asn	Ala	Thr	Ile	
	305					310					315					320	
60	ACG	GAC	ATT	ATC	TCA	GCC	CTG	GTG	ACC	AGC	ACA	TTC	ATC	ATT	GAG	AAG	1008
	Thr	Asp	Ile	Ile	Ser	Ala	Leu	Val	Thr	Ser	Thr	Phe	Ile	Ile	Glu	Lys	
					325					330					335		
65	CAG	CCT	CCT	CAG	GTC	CTG	AAG	ACC	CAG	ACC	AAG	TTT	GCA	GCC	ACC	GTA	1056
	Gln	Pro	Pro	Gln	Val	Leu	Lys	Thr	Gln	Thr	Lys	Phe	Ala	Ala	Thr	Val	
					340				345					350			
70	CGC	CTG	CTG	GTG	GGC	GGG	AAG	CTG	AAC	GTG	CAC	ATG	AAT	CCC	CCC	CAG	1104

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	Arg	Leu	Leu	Val	Gly	Gly	Lys	Leu	Asn	Val	His	Met	Asn	Pro	Pro	Gln	
	355							360					365				
5	GTG	AAG	GCC	ACC	ATC	ATC	AGT	GAG	CAG	CAG	GCC	AAG	TCT	CTG	CTT	AAA	1152
	Val	Lys	Ala	Thr	Ile	Ile	Ser	Glu	Gln	Gln	Ala	Lys	Ser	Leu	Leu	Lys	
	370						375					380					
10	AAT	GAG	AAC	ACC	CGC	AAC	GAG	TGC	AGT	GGT	GAG	ATC	CTG	AAC	AAC	TGC	1200
	Asn	Glu	Asn	Thr	Arg	Asn	Glu	Cys	Ser	Gly	Glu	Ile	Leu	Asn	Asn	Cys	
	385					390					395				400		
15	TGC	GTG	ATG	GAG	TAC	CAC	CAA	GCC	ACG	GGC	ACC	CTC	AGT	GCC	CAC	TTC	1248
	Cys	Val	Met	Glu	Tyr	His	Gln	Ala	Thr	Gly	Thr	Leu	Ser	Ala	His	Phe	
				405						410					415		
	AGG	AAC	ATG	TCA	CTG	AAG	AGG	ATC	AAG	CGT	GCT	GAC	CGG	CGG	GGT	GCA	1296
	Arg	Asn	Met	Ser	Leu	Lys	Arg	Ile	Lys	Arg	Ala	Asp	Arg	Arg	Gly	Ala	
				420					425					430			
20	GAG	TCC	GTG	ACA	GAG	GAG	AAG	TTC	ACA	GTC	CTG	TTT	GAG	TCT	CAG	TTC	1344
	Glu	Ser	Val	Thr	Glu	Glu	Lys	Phe	Thr	Val	Leu	Phe	Glu	Ser	Gln	Phe	
		435						440					445				
25	AGT	GTT	GGC	AGC	AAT	GAG	CTT	GTG	TTC	CAG	GTG	AAG	ACT	CTG	TCC	CTA	1392
	Ser	Val	Gly	Ser	Asn	Glu	Leu	Val	Phe	Gln	Val	Lys	Thr	Leu	Ser	Leu	
	450					455					460						
30	CCT	GTG	GTT	GTC	ATC	GTC	CAC	GGC	AGC	CAG	GAC	CAC	AAT	GCC	ACG	GCT	1440
	Pro	Val	Val	Val	Ile	Val	His	Gly	Ser	Gln	Asp	His	Asn	Ala	Thr	Ala	
	465					470					475				480		
35	ACT	GTG	CTG	TGG	GAC	AAT	GCC	TTT	GCT	GAG	CCG	GGC	AGG	GTG	CCA	TTT	1488
	Thr	Val	Leu	Trp	Asp	Asn	Ala	Phe	Ala	Glu	Pro	Gly	Arg	Val	Pro	Phe	
				485						490					495		
	GCC	GTG	CCT	GAC	AAA	GTG	CTG	TGG	CCG	CAG	CTG	TGT	GAG	GCG	CTC	AAC	1536
	Ala	Val	Pro	Asp	Lys	Val	Leu	Trp	Pro	Gln	Leu	Cys	Glu	Ala	Leu	Asn	
				500					505					510			
40	ATG	AAA	TTC	AAG	GCC	GAA	GTG	CAG	AGC	AAC	CGG	GGC	CTG	ACC	AAG	GAG	1584
	Met	Lys	Phe	Lys	Ala	Glu	Val	Gln	Ser	Asn	Arg	Gly	Leu	Thr	Lys	Glu	
		515						520					525				
45	AAC	CTC	GTG	TTC	CTG	GCG	CAG	AAA	CTG	TTC	AAC	AAC	AGC	AGC	AGC	CAC	1632
	Asn	Leu	Val	Phe	Leu	Ala	Gln	Lys	Leu	Phe	Asn	Asn	Ser	Ser	Ser	His	
	530					535					540						
50	CTG	GAG	GAC	TAC	AGT	GGC	CTG	TCC	GTG	TCC	TGG	TCC	CAG	TTC	AAC	AGG	1680
	Leu	Glu	Asp	Tyr	Ser	Gly	Leu	Ser	Val	Ser	Trp	Ser	Gln	Phe	Asn	Arg	
	545					550					555				560		
55	GAG	AAC	TTG	CCG	GGC	TGG	AAC	TAC	ACC	TTC	TGG	CAG	TGG	TTT	GAC	GGG	1728
	Glu	Asn	Leu	Pro	Gly	Trp	Asn	Tyr	Thr	Phe	Trp	Gln	Trp	Phe	Asp	Gly	
				565						570					575		
	GTG	ATG	GAG	GTG	TTG	AAG	AAG	CAC	CAC	AAG	CCC	CAC	TGG	AAT	GAT	GGG	1776

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	Val	Met	Glu	Val	Leu	Lys	Lys	His	His	Lys	Pro	His	Trp	Asn	Asp	Gly	
				580					585					590			
5	GCC	ATC	CTA	GGT	TTT	GTG	AAT	AAG	CAA	CAG	GCC	CAC	GAC	CTG	CTC	ATC	1824
	Ala	Ile	Leu	Gly	Phe	Val	Asn	Lys	Gln	Gln	Ala	His	Asp	Leu	Leu	Ile	
			595					600					605				
10	AAC	AAG	CCC	GAC	GGG	ACC	TTC	TTG	TTG	CGC	TTT	AGT	GAC	TCA	GAA	ATC	1872
	Asn	Lys	Pro	Asp	Gly	Thr	Phe	Leu	Leu	Arg	Phe	Ser	Asp	Ser	Glu	Ile	
			610				615					620					
15	GGG	GGC	ATC	ACC	ATC	GCC	TGG	AAG	TTT	GAC	TCC	CCG	GAA	CGC	AAC	CTG	1920
	Gly	Gly	Ile	Thr	Ile	Ala	Trp	Lys	Phe	Asp	Ser	Pro	Glu	Arg	Asn	Leu	
	625					630				635					640		
	TGG	AAC	CTG	AAA	CCA	TTC	ACC	ACG	CGG	GAT	TTC	TCC	ATC	AGG	TCC	CTG	1968
	Trp	Asn	Leu	Lys	Pro	Phe	Thr	Thr	Arg	Asp	Phe	Ser	Ile	Arg	Ser	Leu	
				645					650					655			
20	GCT	GAC	CGG	CTG	GGG	GAC	CTG	AGC	TAT	CTC	ATC	TAT	GTG	TTT	CCT	GAC	2016
	Ala	Asp	Arg	Leu	Gly	Asp	Leu	Ser	Tyr	Leu	Ile	Tyr	Val	Phe	Pro	Asp	
				660					665					670			
25	CGC	CCC	AAG	GAT	GAG	GTC	TTC	TCC	AAG	TAC	TAC	ACT	CCT	GTG	CTG	GCT	2064
	Arg	Pro	Lys	Asp	Glu	Val	Phe	Ser	Lys	Tyr	Tyr	Thr	Pro	Val	Leu	Ala	
			675					680					685				
30	AAA	GCT	GTT	GAT	GGA	TAT	GTG	AAA	CCA	CAG	ATC	AAG	CAA	GTG	GTC	CCT	2112
	Lys	Ala	Val	Asp	Gly	Tyr	Val	Lys	Pro	Gln	Ile	Lys	Gln	Val	Val	Pro	
		690					695					700					
35	GAG	TTT	GTG	AAT	GCA	TCT	GCA	GAT	GCT	GGG	GGC	AGC	AGC	GCC	ACG	TAC	2160
	Glu	Phe	Val	Asn	Ala	Ser	Ala	Asp	Ala	Gly	Gly	Ser	Ser	Ala	Thr	Tyr	
	705					710				715					720		
	ATG	GAC	CAG	GCC	CCC	TCC	CCA	GCT	GTG	TGC	CCC	CAG	GCT	CCC	TAT	AAC	2208
	Met	Asp	Gln	Ala	Pro	Ser	Pro	Ala	Val	Cys	Pro	Gln	Ala	Pro	Tyr	Asn	
				725					730					735			
40	ATG	TAC	CCA	CAG	AAC	CCT	GAC	CAT	GTA	CTC	GAT	CAG	GAT	GGA	GAA	TTC	2256
	Met	Tyr	Pro	Gln	Asn	Pro	Asp	His	Val	Leu	Asp	Gln	Asp	Gly	Glu	Phe	
				740				745						750			
45	GAC	CTG	GAT	GAG	ACC	ATG	GAT	GTG	GCC	AGG	CAC	GTG	GAG	GAA	CTC	TTA	2304
	Asp	Leu	Asp	Glu	Thr	Met	Asp	Val	Ala	Arg	His	Val	Glu	Glu	Leu	Leu	
			755					760					765				
50	CGC	CGA	CCA	ATG	GAC	AGT	CTT	GAC	TCC	CGC	CTC	TCG	CCC	CCT	GCC	GGT	2352
	Arg	Arg	Pro	Met	Asp	Ser	Leu	Asp	Ser	Arg	Leu	Ser	Pro	Pro	Ala	Gly	
		770					775					780					
55	CTT	TTC	ACC	TCT	GCC	AGA	GGC	TCC	CTC	TCA	TGG	GTA	CCG	CGG	GCC	CGG	2400
	Leu	Phe	Thr	Ser	Ala	Arg	Gly	Ser	Leu	Ser	Trp	Val	Pro	Arg	Ala	Arg	
	785					790				795					800		
	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	2448

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182																
	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr
					805					810					815	
5	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC
	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His
				820					825					830		
10	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG
	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys
			835					840						845		
15	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG
	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp
			850				855						860			
20	CCC	ACC	CTC	GTG	ACC	ACC	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC
	Pro	Thr	Leu	Val	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	
	865					870				875					880	
25	TAC	CCC	GAC	CAC	ATG	AAG	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC
	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro
				885						890					895	
30	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC
	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn
			900						905					910		
35	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC
	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn
			915					920						925		
40	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG
	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu
		930					935						940			
45	GGG	CAC	AAG	CTG	GAG	TAC	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG
	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met
	945					950					955				960	
50	GCC	GAC	AAG	CAG	AAG	AAC	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC
	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His
				965						970				975		
55	AAC	ATC	GAG	GAC	GGC	AGC	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC
	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn
			980						985					990		
60	ACC	CCC	ATC	GGC	GAC	GGC	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG
	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu
			995					1000					1005			
65	AGC	ACC	CAG	TCC	GCC	CTG	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC
	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His
		1010					1015				1020					
70	ATG	GTC	CTG	CTG	GAG	TTC	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG

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Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met  
 1025 1030 1035 1040

5 GAC GAG CTG TAC AAG TAA 3138  
 Asp Glu Leu Tyr Lys  
 1045

## (2) INFORMATION FOR SEQ ID NO:79:

10

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1045 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15

- (ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ala Gly Trp Ile Gln Ala Gln Gln Leu Gln Gly Asp Ala Leu Arg  
 1 5 10 15  
 Gln Met Gln Val Leu Tyr Gly Gln His Phe Pro Ile Glu Val Arg His  
 25 20 25 30  
 Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp Asp Ala Ile Asp Leu  
 35 40 45  
 Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln Leu Leu Glu Gly Leu  
 50 55 60  
 Val Gln Glu Leu Gln Lys Lys Ala Glu His Gln Val Gly Glu Asp Gly  
 30 65 70 75 80  
 Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala Thr Gln Leu Gln Lys  
 85 90 95  
 Thr Tyr Asp Arg Cys Pro Leu Glu Leu Val Arg Cys Ile Arg His Ile  
 35 100 105 110  
 Leu Tyr Asn Glu Gln Arg Leu Val Arg Glu Ala Asn Asn Cys Ser Ser  
 115 120 125  
 Pro Ala Gly Ile Leu Val Asp Ala Met Ser Gln Lys His Leu Gln Ile  
 130 135 140  
 Asn Gln Thr Phe Glu Glu Leu Arg Leu Val Thr Gln Asp Thr Glu Asn  
 40 145 150 155 160  
 Glu Leu Lys Lys Leu Gln Gln Thr Gln Glu Tyr Phe Ile Ile Gln Tyr  
 165 170 175  
 Gln Glu Ser Leu Arg Ile Gln Ala Gln Phe Ala Gln Leu Ala Gln Leu  
 45 180 185 190  
 Ser Pro Gln Glu Arg Leu Ser Arg Glu Thr Ala Leu Gln Gln Lys Gln  
 195 200 205  
 Val Ser Leu Glu Ala Trp Leu Gln Arg Glu Ala Gln Thr Leu Gln Gln  
 210 215 220  
 Tyr Arg Val Glu Leu Ala Glu Lys His Gln Lys Thr Leu Gln Leu Leu  
 50 225 230 235 240  
 Arg Lys Gln Gln Thr Ile Ile Leu Asp Asp Glu Leu Ile Gln Trp Lys  
 245 250 255  
 Arg Arg Gln Gln Leu Ala Gly Asn Gly Gly Pro Pro Glu Gly Ser Leu  
 55 260 265 270  
 Asp Val Leu Gln Ser Trp Cys Glu Lys Leu Ala Glu Ile Ile Trp Gln

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		275				280				285				
		Asn	Arg	Gln	Gln	Ile	Arg	Arg	Ala	Glu	His	Leu	Cys	Gln
		290							295				300	
		Ile	Pro	Gly	Pro	Val	Glu	Glu	Met	Leu	Ala	Glu	Val	Asn
5		305					310					315		320
		Thr	Asp	Ile	Ile	Ser	Ala	Leu	Val	Thr	Ser	Thr	Phe	Ile
						325					330			335
		Gln	Pro	Pro	Gln	Val	Leu	Lys	Thr	Gln	Thr	Lys	Phe	Ala
						340				345				350
10		Arg	Leu	Leu	Val	Gly	Gly	Lys	Leu	Asn	Val	His	Met	Asn
						355				360				365
		Val	Lys	Ala	Thr	Ile	Ile	Ser	Glu	Gln	Gln	Ala	Lys	Ser
						370				375				380
		Asn	Glu	Asn	Thr	Arg	Asn	Glu	Cys	Ser	Gly	Glu	Ile	Leu
15		385					390					395		400
		Cys	Val	Met	Glu	Tyr	His	Gln	Ala	Thr	Gly	Thr	Leu	Ser
						405					410			415
		Arg	Asn	Met	Ser	Leu	Lys	Arg	Ile	Lys	Arg	Ala	Asp	Arg
						420				425				430
20		Glu	Ser	Val	Thr	Glu	Glu	Lys	Phe	Thr	Val	Leu	Phe	Glu
						435				440				445
		Ser	Val	Gly	Ser	Asn	Glu	Leu	Val	Phe	Gln	Val	Lys	Thr
						450				455				460
		Pro	Val	Val	Val	Ile	Val	His	Gly	Ser	Gln	Asp	His	Asn
25		465					470					475		480
		Thr	Val	Leu	Trp	Asp	Asn	Ala	Phe	Ala	Glu	Pro	Gly	Arg
						485					490			495
		Ala	Val	Pro	Asp	Lys	Val	Leu	Trp	Pro	Gln	Leu	Cys	Glu
						500				505				510
30		Met	Lys	Phe	Lys	Ala	Glu	Val	Gln	Ser	Asn	Arg	Gly	Leu
						515				520				525
		Asn	Leu	Val	Phe	Leu	Ala	Gln	Lys	Leu	Phe	Asn	Asn	Ser
						530				535				540
		Leu	Glu	Asp	Tyr	Ser	Gly	Leu	Ser	Val	Ser	Trp	Ser	Gln
35		545					550					555		560
		Glu	Asn	Leu	Pro	Gly	Trp	Asn	Tyr	Thr	Phe	Trp	Gln	Trp
						565					570			575
		Val	Met	Glu	Val	Leu	Lys	Lys	His	His	Lys	Pro	His	Trp
						580				585				590
40		Ala	Ile	Leu	Gly	Phe	Val	Asn	Lys	Gln	Gln	Ala	His	Asp
						595				600				605
		Asn	Lys	Pro	Asp	Gly	Thr	Phe	Leu	Leu	Arg	Phe	Ser	Asp
						610				615				620
		Gly	Gly	Ile	Thr	Ile	Ala	Trp	Lys	Phe	Asp	Ser	Pro	Glu
45		625					630					635		640
		Trp	Asn	Leu	Lys	Pro	Phe	Thr	Thr	Arg	Asp	Phe	Ser	Ile
						645					650			655
		Ala	Asp	Arg	Leu	Gly	Asp	Leu	Ser	Tyr	Leu	Ile	Tyr	Val
						660				665				670
50		Arg	Pro	Lys	Asp	Glu	Val	Phe	Ser	Lys	Tyr	Tyr	Thr	Pro
						675				680				685
		Lys	Ala	Val	Asp	Gly	Tyr	Val	Lys	Pro	Gln	Ile	Lys	Gln
						690				695				700
		Glu	Phe	Val	Asn	Ala	Ser	Ala	Asp	Ala	Gly	Gly	Ser	Ser
55		705					710				715			720
		Met	Asp	Gln	Ala	Pro	Ser	Pro	Ala	Val	Cys	Pro	Gln	Ala

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185

				725					730					735
	Met	Tyr	Pro	Gln	Asn	Pro	Asp	His	Val	Leu	Asp	Gln	Asp	Gly
				740					745					750
5	Asp	Leu	Asp	Glu	Thr	Met	Asp	Val	Ala	Arg	His	Val	Glu	Glu
			755					760					765	
	Arg	Arg	Pro	Met	Asp	Ser	Leu	Asp	Ser	Arg	Leu	Ser	Pro	Pro
			770				775					780		
	Leu	Phe	Thr	Ser	Ala	Arg	Gly	Ser	Leu	Ser	Trp	Val	Pro	Arg
						790					795			800
10	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu
					805						810			815
	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn
				820					825					830
	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr
15				835					840				845	
	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val
				850			855					860		
	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe
						870					875			880
20	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala
					885					890				895
	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp
				900					905					910
25	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu
				915					920				925	
	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn
				930			935					940		Ile
	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr
						950					955			960
30	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile
					965					970				975
	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln
				980					985					990
35	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His
				995				1000					1005	
	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg
				1010			1015				1020			
	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu
						1030					1035			1040
40	Asp	Glu	Leu	Tyr	Lys									
					1045									

## (2) INFORMATION FOR SEQ ID NO:80:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TGGGATCCTC AGGCCGTGCT GCTGGCCG

55

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## (2) INFORMATION FOR SEQ ID NO:81:

185

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:  
GTCTCGAGGG AGCATGGGCA CCTTGCG 27
- 15 (2) INFORMATION FOR SEQ ID NO:82:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:  
TGGGATCCGA GAAGTCTATA TCCCATC 27
- 25 (2) INFORMATION FOR SEQ ID NO:83:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:  
TGGGATCCTT AGAAGTCTAT ATCCCATC 28
- 35 (2) INFORMATION FOR SEQ ID NO:84:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:  
GTCTCGAGCC ATGAACGCCC CCGAGCGG 28
- 45 (2) INFORMATION FOR SEQ ID NO:85:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid
- 55

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGAATTCTC GTCTGATTTC TGGCAGGAGG

30

(2) INFORMATION FOR SEQ ID NO:86:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

20 GTGAATTCTT TACGTCTGAT TTCTGGCAGG

30

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTCTCGAGCC ATGGACGAAC TGTTCCCCCT CATC

34

35 (2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

40

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

45

GTGGATCCAA GGAGCTGATC TGA CT CAGCA G

31

(2) INFORMATION FOR SEQ ID NO:89:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

55

(D) TOPOLOGY: linear

187

188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTGGATCCTT AGGAGCTGAT CTGACTCAGC AG 32

5 (2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

15 CCTCCTAAGC TTATCATGGA CCATTATGAT TC 32

(2) INFORMATION FOR SEQ ID NO:91:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

30 CCTCCTGGAT CCCTGCGCAG GATGATGGTC CAG 33

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

40 GGATGGAAGC TTCAATGGCT GCCATCCGGA AGAACTGGT GATTG 45

(2) INFORMATION FOR SEQ ID NO:93:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

55 GGATGGGGAT CCTCACAAGA CAAGGCAACC AGATTTTTC TTCCC 45

188



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(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GGGAAGCTTC CATGAGCGAG ACGGTCATC 29

(2) INFORMATION FOR SEQ ID NO:95:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

25 CCCGGATCCT CAGGGAGAAC CCCGCTTC 28

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTGAATTCTGA CCATGGAGCG GCCCCCGGGG 30

40 (2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
45 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

50 GTGGTACCCA TTCTGTTAAC CAACTCC 27

(2) INFORMATION FOR SEQ ID NO:98:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs

189

190

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTGGTACCTC ATTCTGTAA CCAACTCC

28

10

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

20

GTCTCGAGAG ATGCTGTCCC GTGGGTGG

28

(2) INFORMATION FOR SEQ ID NO:100:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTGAATTCGC TTCCTCTTGA GGGAACC

27

35

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTGAATTCAC TTCCTCTTGA GGGAACC

27

50

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

5 GTCTCGAGCC ATGGAGAACT TCCAAAAGG 29

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GTGGATCCCA GAGTCGAAGA TGGGGTAC 28

(2) INFORMATION FOR SEQ ID NO:104:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

30 GTGGATCCTC AGAGTCGAAG ATGGGGTAC 29

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGAATTCGG CGATGCCAGA CCCC GCGGCG 30

45 (2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
50 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTGGATCCCA GGCACAGGCA GCCTCAGCCT TC 32  
191

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 33 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GTGGATCCTC AGGCACAGGC AGCCTCAGCC TTC

33

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 2616 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2613

(D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG 240  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG 288  
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG 336

192

193

	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
5	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	384
	115 120 125	
10	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	432
	130 135 140	
15	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	480
	145 150 155 160	
	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	528
	165 170 175	
20	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	576
	180 185 190	
25	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	624
	195 200 205	
30	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	672
	210 215 220	
35	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	720
	225 230 235 240	
	GGA CTC AGA TCT CGA GCT CAA GCT TCG AAT TCG GCG ATG CCA GAC CCC Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Met Pro Asp Pro	768
	245 250 255	
40	GCG GCG CAC CTG CCC TTC TTC TAC GGC AGC ATC TCG CGT GCC GAG GCC Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser Arg Ala Glu Ala	816
	260 265 270	
45	GAG GAG CAC CTG AAG CTG GCG GGC ATG GCG GAC GGG CTC TTC CTG CTG Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly Leu Phe Leu Leu	864
	275 280 285	
50	CGC CAG TGC CTG CGC TCG CTG GGC GGC TAT GTG CTG TCG CTC GTG CAC Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu Ser Leu Val His	912
	290 295 300	
55	GAT GTG CGC TTC CAC CAC TTT CCC ATC GAG CGC CAG CTC AAC GGC ACC Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln Leu Asn Gly Thr	960
	305 310 315 320	
	TAC GCC ATT GCC GGC GGC AAA GCG CAC TGT GGA CCG GCA GAG CTC TGC	1008

193

194

	Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro Ala Glu Leu Cys	
	325 330 335	
5	GAG TTC TAC TCG CGC GAC CCC GAC GGG CTG CCC TGC AAC CTG CGC AAG Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys Asn Leu Arg Lys	1056
	340 345 350	
10	CCG TGC AAC CGG CCG TCG GGC CTC GAG CCG CAG CCG GGG GTC TTC GAC Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro Gly Val Phe Asp	1104
	355 360 365	
15	TGC CTG CGA GAC GCC ATG GTG CGT GAC TAC GTG CGC CAG ACG TGG AAG Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg Gln Thr Trp Lys	1152
	370 375 380	
20	CTG GAG GGC GAG GCC CTG GAG CAG GCC ATC ATC AGC CAG GCC CCG CAG Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser Gln Ala Pro Gln	1200
	385 390 395 400	
25	GTG GAG AAG CTC ATT GCT ACG ACG GCC CAC GAG CGG ATG CCC TGG TAC Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg Met Pro Trp Tyr	1248
	405 410 415	
30	CAC AGC AGC CTG ACG CGT GAG GAG GCC GAG CGC AAA CTT TAC TCT GGG His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys Leu Tyr Ser Gly	1296
	420 425 430	
35	GCG CAG ACC GAC GGC AAG TTC CTG CTG AGG CCG CGG AAG GAG CAG GGC Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg Lys Glu Gln Gly	1344
	435 440 445	
40	ACA TAC GCC CTG TCC CTC ATC TAT GGG AAG ACG GTG TAC CAC TAC CTC Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val Tyr His Tyr Leu	1392
	450 455 460	
45	ATC AGC CAA GAC AAG GCG GGC AAG TAC TGC ATT CCC GAG GGC ACC AAG Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro Glu Gly Thr Lys	1440
	465 470 475 480	
50	TTT GAC ACG CTC TGG CAG CTG GTG GAG TAT CTG AAG CTG AAG GCG GAC Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys Leu Lys Ala Asp	1488
	485 490 495	
55	GGG CTC ATC TAC TGC CTG AAG GAG GCC TGC CCC AAC AGC AGT GCC AGC Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn Ser Ser Ala Ser	1536
	500 505 510	
60	AAC GCC TCA GGG GCT GCT GCT CCC ACA CTC CCA GCC CAC CCA TCC ACG Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala His Pro Ser Thr	1584
	515 520 525	
65	TTG ACT CAT CCT CAG AGA CGA ATC GAC ACC CTC AAC TCA GAT GGA TAC Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn Ser Asp Gly Tyr	1632
	530 535 540	
70	ACC CCT GAG CCA GCA CGC ATA ACG TCC CCA GAC AAA CCG CGG CCG ATG	1680

194

195

	Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys Pro Arg Pro Met	
	545 550 555 560	
5	CCC ATG GAC ACG AGC GTG TAT GAG AGC CCC TAC AGC GAC CCA GAG GAG Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu	1728
	565 570 575	
10	CTC AAG GAC AAG AAG CTC TTC CTG AAG CGC GAT AAC CTC CTC ATA GCT Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn Leu Leu Ile Ala	1776
	580 585 590	
15	GAC ATT GAA CTT GGC TGC GGC AAC TTT GGC TCA GTG CGC CAG GGC GTG Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val Arg Gln Gly Val	1824
	595 600 605	
	TAC CGC ATG CGC AAG AAG CAG ATC GAC GTG GCC ATC AAG GTG CTG AAG Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys	1872
	610 615 620	
20	CAG GGC ACG GAG AAG GCA GAC ACG GAA GAG ATG ATG CGC GAG GCG CAG Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln	1920
	625 630 635 640	
25	ATC ATG CAC CAG CTG GAC AAC CCC TAC ATC GTG CGG CTC ATT GGC GTC Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val	1968
	645 650 655	
30	TGC CAG GCC GAG GCC CTC ATG CTG GTC ATG GAG ATG GCT GGG GGC GGG Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met Ala Gly Gly Gly	2016
	660 665 670	
35	CCG CTG CAC AAG TTC CTG GTC GGC AAG AGG GAG GAG ATC CCT GTG AGC Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser	2064
	675 680 685	
	AAT GTG GCC GAG CTG CTG CAC CAG GTG TCC ATG GGG ATG AAG TAC CTG Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly Met Lys Tyr Leu	2112
	690 695 700	
40	GAG GAG AAG AAC TTT GTG CAC CGT GAC CTG GCG GCC CGC AAC GTC CTG Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val Leu	2160
	705 710 715 720	
45	CTG GTT AAC CGG CAC TAC GCC AAG ATC AGC GAC TTT GGC CTC TCC AAA Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys	2208
	725 730 735	
50	GCA CTG GGT GCC GAC GAC AGC TAC TAC ACT GCC CGC TCA GCA GGG AAG Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys	2256
	740 745 750	
55	TGG CCG CTC AAG TGG TAC GCA CCC GAA TGC ATC AAC TTC CGC AAG TTC Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe	2304
	755 760 765	
	TCC AGC CGC AGC GAT GTC TGG AGC TAT GGG GTC ACC ATG TGG GAG GCC	2352

195

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	Ser	Ser	Arg	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Met	Trp	Glu	Ala	
	770						775					780					
5	TTG	TCC	TAC	GGC	CAG	AAG	CCC	TAC	AAG	AAG	ATG	AAA	GGG	CCG	GAG	GTC	2400
	Leu	Ser	Tyr	Gly	Gln	Lys	Pro	Tyr	Lys	Lys	Met	Lys	Gly	Pro	Glu	Val	
	785					790					795					800	
10	ATG	GCC	TTC	ATC	GAG	CAG	GGC	AAG	CGG	ATG	GAG	TGC	CCA	CCA	GAG	TGT	2448
	Met	Ala	Phe	Ile	Glu	Gln	Gly	Lys	Arg	Met	Glu	Cys	Pro	Pro	Glu	Cys	
					805					810						815	
15	CCA	CCC	GAA	CTG	TAC	GCA	CTC	ATG	AGT	GAC	TGC	TGG	ATC	TAC	AAG	TGG	2496
	Pro	Pro	Glu	Leu	Tyr	Ala	Leu	Met	Ser	Asp	Cys	Trp	Ile	Tyr	Lys	Trp	
					820				825						830		
20	GAG	GAT	CGC	CCC	GAC	TTC	CTG	ACC	GTG	GAG	CAG	CGC	ATG	CGA	GCC	TGT	2544
	Glu	Asp	Arg	Pro	Asp	Phe	Leu	Thr	Val	Glu	Gln	Arg	Met	Arg	Ala	Cys	
			835						840					845			
25	TAC	TAC	AGC	CTG	GCC	AGC	AAG	GTG	GAA	GGG	CCC	CCA	GGC	AGC	ACA	CAG	2592
	Tyr	Tyr	Ser	Leu	Ala	Ser	Lys	Val	Glu	Gly	Pro	Pro	Gly	Ser	Thr	Gln	
			850					855								860	
30	AAG	GCT	GAG	GCT	GCC	TGT	GCC	TGA									2616
	Lys	Ala	Glu	Ala	Ala	Cys	Ala										
	865						870										

## (2) INFORMATION FOR SEQ ID NO:109:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 871 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10					15		
45	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35					40					45				
	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
		50					55					60					
50	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70					75					80	
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85					90					95		
55	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	

196



197

115 120 125  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 5 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190  
 10 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
 195 200 205  
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220  
 15 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser  
 225 230 235 240  
 Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Met Pro Asp Pro  
 245 250 255  
 Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser Arg Ala Glu Ala  
 260 265 270  
 20 Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly Leu Phe Leu Leu  
 275 280 285  
 Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu Ser Leu Val His  
 290 295 300  
 25 Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln Leu Asn Gly Thr  
 305 310 315 320  
 Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro Ala Glu Leu Cys  
 325 330 335  
 Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys Asn Leu Arg Lys  
 340 345 350  
 30 Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro Gly Val Phe Asp  
 355 360 365  
 Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg Gln Thr Trp Lys  
 370 375 380  
 35 Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser Gln Ala Pro Gln  
 385 390 395 400  
 Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg Met Pro Trp Tyr  
 405 410 415  
 His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys Leu Tyr Ser Gly  
 420 425 430  
 40 Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg Lys Glu Gln Gly  
 435 440 445  
 Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val Tyr His Tyr Leu  
 450 455 460  
 45 Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro Glu Gly Thr Lys  
 465 470 475 480  
 Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys Leu Lys Ala Asp  
 485 490 495  
 Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn Ser Ser Ala Ser  
 500 505 510  
 50 Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala His Pro Ser Thr  
 515 520 525  
 Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn Ser Asp Gly Tyr  
 530 535 540  
 55 Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys Pro Arg Pro Met  
 545 550 555 560  
 Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu

197

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		565		570		575
	Leu	Lys	Asp	Lys	Lys	Leu
				Phe	Leu	Lys
				Arg	Asp	Asn
				Leu	Leu	Ile
				Ala		
		580		585		590
	Asp	Ile	Glu	Leu	Gly	Cys
				Gly	Asn	Phe
				Gly	Ser	Val
				Arg	Gln	Gly
5		595		600		605
	Tyr	Arg	Met	Arg	Lys	Lys
				Gln	Ile	Asp
				Val	Ala	Ile
				Lys	Val	Leu
		610		615		620
	Gln	Gly	Thr	Glu	Lys	Ala
				Asp	Thr	Glu
				Glu	Glu	Met
				Arg	Glu	Ala
		625		630		635
				640		
10	Ile	Met	His	Gln	Leu	Asp
				Asn	Pro	Tyr
				Ile	Val	Arg
				Leu	Ile	Gly
				Val		
		645		650		655
	Cys	Gln	Ala	Glu	Ala	Leu
				Met	Leu	Val
				Met	Glu	Met
				Ala	Gly	Gly
		660		665		670
	Pro	Leu	His	Lys	Phe	Leu
				Val	Gly	Lys
				Arg	Glu	Glu
				Ile	Pro	Val
		675		680		685
15	Asn	Val	Ala	Glu	Leu	Leu
				His	Gln	Val
				Ser	Met	Gly
				Met	Lys	Tyr
		690		695		700
	Glu	Glu	Lys	Asn	Phe	Val
				His	Arg	Asp
				Leu	Ala	Ala
				Arg	Asn	Val
		705		710		715
				720		
20	Leu	Val	Asn	Arg	His	Tyr
				Ala	Lys	Ile
				Ser	Asp	Phe
				Gly	Leu	Ser
				Lys		
		725		730		735
	Ala	Leu	Gly	Ala	Asp	Asp
				Ser	Tyr	Tyr
				Thr	Ala	Arg
				Ser	Ala	Gly
		740		745		750
	Trp	Pro	Leu	Lys	Trp	Tyr
				Ala	Pro	Glu
				Cys	Ile	Asn
				Phe	Arg	Lys
		755		760		765
25	Ser	Ser	Arg	Ser	Asp	Val
				Trp	Ser	Tyr
				Gly	Val	Thr
				Met	Trp	Glu
		770		775		780
	Leu	Ser	Tyr	Gly	Gln	Lys
				Pro	Tyr	Lys
				Lys	Met	Lys
				Gly	Pro	Glu
		785		790		800
30	Met	Ala	Phe	Ile	Glu	Gln
				Gly	Lys	Arg
				Met	Glu	Cys
				Pro	Pro	Glu
				Cys		
		805		810		815
	Pro	Pro	Glu	Leu	Tyr	Ala
				Leu	Met	Ser
				Asp	Cys	Trp
				Ile	Tyr	Lys
		820		825		830
	Glu	Asp	Arg	Pro	Asp	Phe
				Leu	Thr	Val
				Glu	Gln	Arg
		835		840		845
35	Tyr	Tyr	Ser	Leu	Ala	Ser
				Lys	Val	Glu
				Gly	Pro	Pro
				Gly	Ser	Thr
		850		855		860
	Lys	Ala	Glu	Ala	Ala	Cys
				Ala		
		865		870		

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2598 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...2595  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

199

5	ATG CCA GAC CCC GCG GCG CAC CTG CCC TTC TTC TAC GGC AGC ATC TCG Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser 1 5 10 15	48
10	CGT GCC GAG GCC GAG GAG CAC CTG AAG CTG GCG GGC ATG GCG GAC GGG Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly 20 25 30	96
15	CTC TTC CTG CTG CGC CAG TGC CTG CGC TCG CTG GGC GGC TAT GTG CTG Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu 35 40 45	144
20	TCG CTC GTG CAC GAT GTG CGC TTC CAC CAC TTT CCC ATC GAG CGC CAG Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln 50 55 60	192
25	CTC AAC GGC ACC TAC GCC ATT GCC GGC GGC AAA GCG CAC TGT GGA CCG Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro 65 70 75 80	240
30	GCA GAG CTC TGC GAG TTC TAC TCG CGC GAC CCC GAC GGC CTG CCC TGC Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys 85 90 95	288
35	AAC CTG CGC AAG CCG TGC AAC CGG CCG TCG GGC CTC GAG CCG CAG CCG Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro 100 105 110	336
40	GGG GTC TTC GAC TGC CTG CGA GAC GCC ATG GTG CGT GAC TAC GTG CGC Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg 115 120 125	384
45	CAG ACG TGG AAG CTG GAG GGC GAG GCC CTG GAG CAG GCC ATC ATC AGC Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser 130 135 140	432
50	CAG GCC CCG CAG GTG GAG AAG CTC ATT GCT ACG ACG GCC CAC GAG CGG Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg 145 150 155 160	480
55	ATG CCC TGG TAC CAC AGC AGC CTG ACG CGT GAG GAG GCC GAG CGC AAA Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys 165 170 175	528
60	CTT TAC TCT GGG GCG CAG ACC GAC GGC AAG TTC CTG CTG AGG CCG CGG Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg 180 185 190	576
65	AAG GAG CAG GGC ACA TAC GCC CTG TCC CTC ATC TAT GGG AAG ACG GTG Lys Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val 195 200 205	624
70	TAC CAC TAC CTC ATC AGC CAA GAC AAG GCG GGC AAG TAC TGC ATT CCC Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro 210 215 220	672

199

200

5	GAG GGC ACC AAG TTT GAC ACG CTC TGG CAG CTG GTG GAG TAT CTG AAG Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys 225 230 235 240	720
10	CTG AAG GCG GAC GGG CTC ATC TAC TGC CTG AAG GAG GCC TGC CCC AAC Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn 245 250 255	768
15	AGC AGT GCC AGC AAC GCC TCA GGG GCT GCT GCT CCC ACA CTC CCA GCC Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala 260 265 270	816
20	CAC CCA TCC ACG TTG ACT CAT CCT CAG AGA CGA ATC GAC ACC CTC AAC His Pro Ser Thr Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn 275 280 285	864
25	TCA GAT GGA TAC ACC CCT GAG CCA GCA CGC ATA ACG TCC CCA GAC AAA Ser Asp Gly Tyr Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys 290 295 300	912
30	CCG CGG CCG ATG CCC ATG GAC ACG AGC GTG TAT GAG AGC CCC TAC AGC Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser 305 310 315 320	960
35	GAC CCA GAG GAG CTC AAG GAC AAG AAG CTC TTC CTG AAG CGC GAT AAC Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn 325 330 335	1008
40	CTC CTC ATA GCT GAC ATT GAA CTT GGC TGC GGC AAC TTT GGC TCA GTG Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val 340 345 350	1056
45	CGC CAG GGC GTG TAC CGC ATG CGC AAG AAG CAG ATC GAC GTG GCC ATC Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile 355 360 365	1104
50	AAG GTG CTG AAG CAG GGC ACG GAG AAG GCA GAC ACG GAA GAG ATG ATG Lys Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met 370 375 380	1152
55	CGC GAG GCG CAG ATC ATG CAC CAG CTG GAC AAC CCC TAC ATC GTG CGG Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg 385 390 395 400	1200
60	CTC ATT GGC GTC TGC CAG GCC GAG GCC CTC ATG CTG GTC ATG GAG ATG Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met 405 410 415	1248
65	GCT GGG GGC GGG CCG CTG CAC AAG TTC CTG GTC GGC AAG AGG GAG GAG Ala Gly Gly Gly Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu 420 425 430	1296
70	ATC CCT GTG AGC AAT GTG GCC GAG CTG CTG CAC CAG GTG TCC ATG GGG Ile Pro Val Ser Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly 435 440 445	1344

200

5	ATG AAG TAC CTG GAG GAG AAG AAC TTT GTG CAC CGT GAC CTG GCG GCC	1392
	Met Lys Tyr Leu Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala	
	450 455 460	
	CGC AAC GTC CTG CTG GTT AAC CGG CAC TAC GCC AAG ATC AGC GAC TTT	1440
	Arg Asn Val Leu Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe	
10	465 470 475 480	
	GGC CTC TCC AAA GCA CTG GGT GCC GAC GAC AGC TAC TAC ACT GCC CGC	1488
	Gly Leu Ser Lys Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg	
	485 490 495	
	TCA GCA GGG AAG TGG CCG CTC AAG TGG TAC GCA CCC GAA TGC ATC AAC	1536
15	Ser Ala Gly Lys Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn	
	500 505 510	
	TTC CGC AAG TTC TCC AGC CGC AGC GAT GTC TGG AGC TAT GGG GTC ACC	1584
	Phe Arg Lys Phe Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr	
	515 520 525	
20	ATG TGG GAG GCC TTG TCC TAC GGC CAG AAG CCC TAC AAG AAG ATG AAA	1632
	Met Trp Glu Ala Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys	
	530 535 540	
	GGG CCG GAG GTC ATG GCC TTC ATC GAG CAG GGC AAG CCG ATG GAG TGC	1680
	Gly Pro Glu Val Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys	
25	545 550 555 560	
	CCA CCA GAG TGT CCA CCC GAA CTG TAC GCA CTC ATG AGT GAC TGC TGG	1728
	Pro Pro Glu Cys Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp	
	565 570 575	
	ATC TAC AAG TGG GAG GAT CGC CCC GAC TTC CTG ACC GTG GAG CAG CGC	1776
30	Ile Tyr Lys Trp Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg	
	580 585 590	
	ATG CGA GCC TGT TAC TAC AGC CTG GCC AGC AAG GTG GAA GGG CCC CCA	1824
	Met Arg Ala Cys Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro	
	595 600 605	
35	GGC AGC ACA CAG AAG GCT GAG GCT GCC TGT GCC TGG GAT CCA CCG GTC	1872
	Gly Ser Thr Gln Lys Ala Glu Ala Ala Cys Ala Trp Asp Pro Pro Val	
	610 615 620	
	GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC	1920
	Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro	
40	625 630 635 640	
	ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG	1968
	Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val	
	645 650 655	
	TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG	2016
45	Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys	
	660 665 670	
50		
55		

202

	TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG	2064
	Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val	
	675 680 685	
5	ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC	2112
	Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His	
	690 695 700	
10	ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC	2160
	Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val	
	705 710 715 720	
15	CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC	2208
	Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg	
	725 730 735	
20	GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG	2256
	Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu	
	740 745 750	
25	AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG	2304
	Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu	
	755 760 765	
30	GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG	2352
	Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
	770 775 780	
35	AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC	2400
	Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
	785 790 795 800	
40	GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC	2448
	Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
	805 810 815	
45	GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC	2496
	Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser	
	820 825 830	
50	GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG	2544
	Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
	835 840 845	
55	GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC	2592
	Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
	850 855 860	
60	AAG TAA	2598
	Lys	
	865	

55 (2) INFORMATION FOR SEQ ID NO:111:

202

203

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser  
 1 5 10 15  
 Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly  
 15 20 25 30  
 Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu  
 35 40 45  
 Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln  
 50 55 60  
 Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro  
 65 70 75 80  
 Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys  
 85 90 95  
 Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro  
 100 105 110  
 Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg  
 115 120 125  
 Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser  
 130 135 140  
 Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg  
 145 150 155 160  
 Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys  
 165 170 175  
 Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg  
 180 185 190  
 Lys Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val  
 195 200 205  
 Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro  
 210 215 220  
 Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys  
 225 230 235 240  
 Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn  
 245 250 255  
 Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala  
 260 265 270  
 His Pro Ser Thr Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn  
 275 280 285  
 Ser Asp Gly Tyr Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys  
 290 295 300  
 Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser  
 305 310 315 320  
 Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn  
 325 330 335  
 Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val  
 340 345 350  
 Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile

203

204

[illegible]

204



205

805 810 815  
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser  
 820 825 830  
 5 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu  
 835 840 845  
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr  
 850 855 860  
 Lys  
 865

10

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 1635 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...1632  
 (D) OTHER INFORMATION:

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

30	ATG GAG AAC TTC CAA AAG GTG GAA AAG ATC GGA GAG GGC ACG TAC GGA Met Glu Asn Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly 1 5 10 15	48
35	GTT GTG TAC AAA GCC AGA AAC AAG TTG ACG GGA GAG GTG GTG GCG CTT Val Val Tyr Lys Ala Arg Asn Lys Leu Thr Gly Glu Val Val Ala Leu 20 25 30	96
40	AAG AAA ATC CGC CTG GAC ACT GAG ACT GAG GGT GTG CCC AGT ACT GCC Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu Gly Val Pro Ser Thr Ala 35 40 45	144
45	ATC CGA GAG ATC TCT CTG CTT AAG GAG CTT AAC CAT CCT AAT ATT GTC Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Asn His Pro Asn Ile Val 50 55 60	192
50	AAG CTG CTG GAT GTC ATT CAC ACA GAA AAT AAA CTC TAC CTG GTT TTT Lys Leu Leu Asp Val Ile His Thr Glu Asn Lys Leu Tyr Leu Val Phe 65 70 75 80	240
55	GAA TTT CTG CAC CAA GAT CTC AAG AAA TTC ATG GAT GCC TCT GCT CTC Glu Phe Leu His Gln Asp Leu Lys Lys Phe Met Asp Ala Ser Ala Leu 85 90 95	288
	ACT GGC ATT CCT CTT CCC CTC ATC AAG AGC TAT CTG TTC CAG CTG CTC Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu 100 105 110	336
	CAG GGC CTA GCT TTC TGC CAT TCT CAT CGG GTC CTC CAC CGA GAC CTT	384

205

206

	Gln	Gly	Leu	Ala	Phe	Cys	His	Ser	His	Arg	Val	Leu	His	Arg	Asp	Leu	
			115					120					125				
5	AAA	CCT	CAG	AAT	CTG	CTT	ATT	AAC	ACA	GAG	GGG	GCC	ATC	AAG	CTA	GCA	432
	Lys	Pro	Gln	Asn	Leu	Leu	Ile	Asn	Thr	Glu	Gly	Ala	Ile	Lys	Leu	Ala	
		130					135				140						
10	GAC	TTT	GGA	CTA	GCC	AGA	GCT	TTT	GGA	GTC	CCT	GTT	CGT	ACT	TAC	ACC	480
	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Phe	Gly	Val	Pro	Val	Arg	Thr	Tyr	Thr	
	145					150					155					160	
15	CAT	GAG	GTG	GTG	ACC	CTG	TGG	TAC	CGA	GCT	CCT	GAA	ATC	CTC	CTG	GGC	528
	His	Glu	Val	Val	Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Leu	Leu	Gly	
					165					170					175		
20	TCG	AAA	TAT	TAT	TCC	ACA	GCT	GTG	GAC	ATC	TGG	AGC	CTG	GGC	TGC	ATC	576
	Ser	Lys	Tyr	Tyr	Ser	Thr	Ala	Val	Asp	Ile	Trp	Ser	Leu	Gly	Cys	Ile	
			180						185					190			
25	TTT	GCT	GAG	ATG	GTG	ACT	CGC	CGG	GCC	CTG	TTC	CCT	GGA	GAT	TCT	GAG	624
	Phe	Ala	Glu	Met	Val	Thr	Arg	Arg	Ala	Leu	Phe	Pro	Gly	Asp	Ser	Glu	
		195						200					205				
30	ATT	GAC	CAG	CTC	TTC	CGG	ATC	TTT	CGG	ACT	CTG	GGG	ACC	CCA	GAT	GAG	672
	Ile	Asp	Gln	Leu	Phe	Arg	Ile	Phe	Arg	Thr	Leu	Gly	Thr	Pro	Asp	Glu	
		210					215					220					
35	GTG	GTG	TGG	CCA	GGA	GTT	ACT	TCT	ATG	CCT	GAT	TAC	AAG	CCA	AGT	TTC	720
	Val	Val	Trp	Pro	Gly	Val	Thr	Ser	Met	Pro	Asp	Tyr	Lys	Pro	Ser	Phe	
	225					230					235					240	
40	CCC	AAG	TGG	GCC	CGG	CAA	GAT	TTT	AGT	AAA	GTT	GTA	CCT	CCC	CTG	GAT	768
	Pro	Lys	Trp	Ala	Arg	Gln	Asp	Phe	Ser	Lys	Val	Val	Pro	Pro	Leu	Asp	
				245						250					255		
45	GAA	GAT	GGA	CGG	AGC	TTG	TTA	TCG	CAA	ATG	CTG	CAC	TAC	GAC	CCT	AAC	816
	Glu	Asp	Gly	Arg	Ser	Leu	Leu	Ser	Gln	Met	Leu	His	Tyr	Asp	Pro	Asn	
			260					265					270				
50	AAG	CGG	ATT	TCG	GCC	AAG	GCA	GCC	CTG	GCT	CAC	CCT	TTC	TTC	CAG	GAT	864
	Lys	Arg	Ile	Ser	Ala	Lys	Ala	Ala	Leu	Ala	His	Pro	Phe	Phe	Gln	Asp	
		275						280					285				
55	GTG	ACC	AAG	CCA	GTA	CCC	CAT	CTT	CGA	CTC	TGG	GAT	CCA	CCG	GTC	GCC	912
	Val	Thr	Lys	Pro	Val	Pro	His	Leu	Arg	Leu	Trp	Asp	Pro	Pro	Val	Ala	
		290					295					300					
60	ACC	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	960
	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	
	305					310					315				320		
65	CTG	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	1008
	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	
				325						330					335		
70	GGC	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	1056

206

207

	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	
				340					345					350			
5	ATC	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	1104
	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	
			355				360						365				
10	ACC	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	1152
	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	
			370				375					380					
15	AAG	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	1200
	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	
	385				390				395						400		
20	GAG	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	1248
	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	
				405					410						415		
25	GAG	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	1296
	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	
				420					425					430			
30	GGC	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	1344
	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	
			435					440					445				
35	TAC	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	1392
	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	
		450					455					460					
40	AAC	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	1440
	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	
	465				470					475				480			
45	AGC	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	1488
	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	
				485					490					495			
50	GGC	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	1536
	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	
				500					505					510			
55	CTG	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	1584
	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	
			515				520						525				
60	TTC	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	1633
	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	
		530					535					540					
	AA																1635

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

207

208

(A) LENGTH: 544 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

10

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Met Glu Asn Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly
 1           5           10           15
Val Val Tyr Lys Ala Arg Asn Lys Leu Thr Gly Glu Val Val Ala Leu
          20           25           30
15 Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu Gly Val Pro Ser Thr Ala
    35           40           45
Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Asn His Pro Asn Ile Val
   50           55           60
Lys Leu Leu Asp Val Ile His Thr Glu Asn Lys Leu Tyr Leu Val Phe
20 65           70           75           80
Glu Phe Leu His Gln Asp Leu Lys Lys Phe Met Asp Ala Ser Ala Leu
    85           90           95
Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu
   100          105          110
25 Gln Gly Leu Ala Phe Cys His Ser His Arg Val Leu His Arg Asp Leu
    115          120          125
Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu Gly Ala Ile Lys Leu Ala
   130          135          140
Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Val Arg Thr Tyr Thr
30 145          150          155          160
His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu Leu Gly
    165          170          175
Ser Lys Tyr Tyr Ser Thr Ala Val Asp Ile Trp Ser Leu Gly Cys Ile
   180          185          190
35 Phe Ala Glu Met Val Thr Arg Arg Ala Leu Phe Pro Gly Asp Ser Glu
    195          200          205
Ile Asp Gln Leu Phe Arg Ile Phe Arg Thr Leu Gly Thr Pro Asp Glu
   210          215          220
Val Val Trp Pro Gly Val Thr Ser Met Pro Asp Tyr Lys Pro Ser Phe
40 225          230          235          240
Pro Lys Trp Ala Arg Gln Asp Phe Ser Lys Val Val Pro Pro Leu Asp
    245          250          255
Glu Asp Gly Arg Ser Leu Leu Ser Gln Met Leu His Tyr Asp Pro Asn
   260          265          270
45 Lys Arg Ile Ser Ala Lys Ala Ala Leu Ala His Pro Phe Phe Gln Asp
    275          280          285
Val Thr Lys Pro Val Pro His Leu Arg Leu Trp Asp Pro Pro Val Ala
   290          295          300
Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
50 305          310          315          320
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
    325          330          335
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
   340          345          350
55 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
    355          360          365

```

208

209

Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met  
 370 375 380  
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln  
 385 390 395 400  
 5 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala  
 405 410 415  
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys  
 420 425 430  
 10 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu  
 435 440 445  
 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys  
 450 455 460  
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly  
 465 470 475 480  
 15 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp  
 485 490 495  
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala  
 500 505 510  
 20 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu  
 515 520 525  
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 530 535 540

## (2) INFORMATION FOR SEQ ID NO:114:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1635 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

35

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...1632  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

40

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG 48  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

45

GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

50

GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

55

TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

209

210																	
	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	240
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70					75					80	
5	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	288
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85					90					95		
10	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
15	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
20	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130					135					140					
25	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
		145				150					155					160	
30	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165					170						175		
35	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185						190		
40	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195					200					205				
45	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210				215						220					
50	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
		225				230				235						240	
55	GGA	CTC	AGA	TCT	CGA	GCC	ATG	GAG	AAC	TTC	CAA	AAG	GTG	GAA	AAG	ATC	768
	Gly	Leu	Arg	Ser	Arg	Ala	Met	Glu	Asn	Phe	Gln	Lys	Val	Glu	Lys	Ile	
				245					250						255		
50	GGA	GAG	GGC	ACG	TAC	GGA	GTT	GTG	TAC	AAA	GCC	AGA	AAC	AAG	TTG	ACG	816
	Gly	Glu	Gly	Thr	Tyr	Gly	Val	Val	Tyr	Lys	Ala	Arg	Asn	Lys	Leu	Thr	
			260					265						270			
55	GGA	GAG	GTG	GTG	GCG	CTT	AAG	AAA	ATC	CGC	CTG	GAC	ACT	GAG	ACT	GAG	864
	Gly	Glu	Val	Val	Ala	Leu	Lys	Lys	Ile	Arg	Leu	Asp	Thr	Glu	Thr	Glu	
			275					280						285			

211

	GGT GTG CCC AGT ACT GCC ATC CGA GAG ATC TCT CTG CTT AAG GAG CTT	912
	Gly Val Pro Ser Thr Ala Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu	
	290 295 300	
5	AAC CAT CCT AAT ATT GTC AAG CTG CTG GAT GTC ATT CAC ACA GAA AAT	960
	Asn His Pro Asn Ile Val Lys Leu Leu Asp Val Ile His Thr Glu Asn	
	305 310 315 320	
10	AAA CTC TAC CTG GTT TTT GAA TTT CTG CAC CAA GAT CTC AAG AAA TTC	1008
	Lys Leu Tyr Leu Val Phe Glu Phe Leu His Gln Asp Leu Lys Lys Phe	
	325 330 335	
15	ATG GAT GCC TCT GCT CTC ACT GGC ATT CCT CTT CCC CTC ATC AAG AGC	1056
	Met Asp Ala Ser Ala Leu Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser	
	340 345 350	
20	TAT CTG TTC CAG CTG CTC CAG GGC CTA GCT TTC TGC CAT TCT CAT CGG	1104
	Tyr Leu Phe Gln Leu Leu Gln Gly Leu Ala Phe Cys His Ser His Arg	
	355 360 365	
25	GTC CTC CAC CGA GAC CTT AAA CCT CAG AAT CTG CTT ATT AAC ACA GAG	1152
	Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu	
	370 375 380	
30	GGG GCC ATC AAG CTA GCA GAC TTT GGA CTA GCC AGA GCT TTT GGA GTC	1200
	Gly Ala Ile Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Val	
	385 390 395 400	
35	CCT GTT CGT ACT TAC ACC CAT GAG GTG GTG ACC CTG TGG TAC CGA GCT	1248
	Pro Val Arg Thr Tyr Thr His Glu Val Val Thr Leu Trp Tyr Arg Ala	
	405 410 415	
40	CCT GAA ATC CTC CTG GGC TCG AAA TAT TAT TCC ACA GCT GTG GAC ATC	1296
	Pro Glu Ile Leu Leu Gly Ser Lys Tyr Tyr Ser Thr Ala Val Asp Ile	
	420 425 430	
45	TGG AGC CTG GGC TGC ATC TTT GCT GAG ATG GTG ACT CGC CGG GCC CTG	1344
	Trp Ser Leu Gly Cys Ile Phe Ala Glu Met Val Thr Arg Arg Ala Leu	
	435 440 445	
50	TTC CCT GGA GAT TCT GAG ATT GAC CAG CTC TTC CGG ATC TTT CGG ACT	1392
	Phe Pro Gly Asp Ser Glu Ile Asp Gln Leu Phe Arg Ile Phe Arg Thr	
	450 455 460	
55	CTG GGG ACC CCA GAT GAG GTG GTG TGG CCA GGA GTT ACT TCT ATG CCT	1440
	Leu Gly Thr Pro Asp Glu Val Val Trp Pro Gly Val Thr Ser Met Pro	
	465 470 475 480	
60	GAT TAC AAG CCA AGT TTC CCC AAG TGG GCC CGG CAA GAT TTT AGT AAA	1488
	Asp Tyr Lys Pro Ser Phe Pro Lys Trp Ala Arg Gln Asp Phe Ser Lys	
	485 490 495	
65	GTT GTA CCT CCC CTG GAT GAA GAT GGA CGG AGC TTG TTA TCG CAA ATG	1536
	Val Val Pro Pro Leu Asp Glu Asp Gly Arg Ser Leu Leu Ser Gln Met	
	500 505 510	

211

212

CTG CAC TAC GAC CCT AAC AAG CGG ATT TCG GCC AAG GCA GCC CTG GCT 1584  
 Leu His Tyr Asp Pro Asn Lys Arg Ile Ser Ala Lys Ala Ala Leu Ala  
 515 520 525

5 CAC CCT TTC TTC CAG GAT GTG ACC AAG CCA GTA CCC CAT CTT CGA CTC T 1633  
 His Pro Phe Phe Gln Asp Val Thr Lys Pro Val Pro His Leu Arg Leu  
 530 535 540

GA 1635

10

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 544 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

25 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 30 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 35 85 90 95  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 40 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 45 165 170 175  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190  
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
 195 200 205  
 50 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220  
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser  
 225 230 235 240  
 Gly Leu Arg Ser Arg Ala Met Glu Asn Phe Gln Lys Val Glu Lys Ile  
 55 245 250 255  
 Gly Glu Gly Thr Tyr Gly Val Val Tyr Lys Ala Arg Asn Lys Leu Thr

212



213

260 265 270  
 Gly Glu Val Val Ala Leu Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu  
 275 280 285  
 Gly Val Pro Ser Thr Ala Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu  
 290 295 300  
 Asn His Pro Asn Ile Val Lys Leu Leu Asp Val Ile His Thr Glu Asn  
 305 310 315 320  
 Lys Leu Tyr Leu Val Phe Glu Phe Leu His Gln Asp Leu Lys Lys Phe  
 325 330 335  
 10 Met Asp Ala Ser Ala Leu Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser  
 340 345 350  
 Tyr Leu Phe Gln Leu Leu Gln Gly Leu Ala Phe Cys His Ser His Arg  
 355 360 365  
 Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu  
 15 370 375 380  
 Gly Ala Ile Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Val  
 385 390 395 400  
 Pro Val Arg Thr Tyr Thr His Glu Val Val Thr Leu Trp Tyr Arg Ala  
 405 410 415  
 20 Pro Glu Ile Leu Leu Gly Ser Lys Tyr Tyr Ser Thr Ala Val Asp Ile  
 420 425 430  
 Trp Ser Leu Gly Cys Ile Phe Ala Glu Met Val Thr Arg Arg Ala Leu  
 435 440 445  
 Phe Pro Gly Asp Ser Glu Ile Asp Gln Leu Phe Arg Ile Phe Arg Thr  
 25 450 455 460  
 Leu Gly Thr Pro Asp Glu Val Val Trp Pro Gly Val Thr Ser Met Pro  
 465 470 475 480  
 Asp Tyr Lys Pro Ser Phe Pro Lys Trp Ala Arg Gln Asp Phe Ser Lys  
 485 490 495  
 30 Val Val Pro Pro Leu Asp Glu Asp Gly Arg Ser Leu Leu Ser Gln Met  
 500 505 510  
 Leu His Tyr Asp Pro Asn Lys Arg Ile Ser Ala Lys Ala Ala Leu Ala  
 515 520 525  
 His Pro Phe Phe Gln Asp Val Thr Lys Pro Val Pro His Leu Arg Leu  
 35 530 535 540

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 2532 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- 45 (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...2529  
 50 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

55 ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG  
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15

48

213

214

	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
5	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
10	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
15	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
20	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
25	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
30	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
35	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
40	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
45	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
50	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC	576
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
55	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG	624
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
	195 200 205	
60	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC	672
	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
	210 215 220	
65	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC	720
	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	

214

215

	GGA CTC AGA TCT CGA GAG ATG CTG TCC CGT GGG TGG TTT CAC CGA GAC	768
	Gly Leu Arg Ser Arg Glu Met Leu Ser Arg Gly Trp Phe His Arg Asp	
	245 250 255	
5	CTC AGT GGG CTG GAT GCA GAG ACC CTG CTC AAG GGC CGA GGT GTC CAC	816
	Leu Ser Gly Leu Asp Ala Glu Thr Leu Leu Lys Gly Arg Gly Val His	
	260 265 270	
10	GGT AGC TTC CTG GCT CGG CCC AGT CGC AAG AAC CAG GGT GAC TTC TCG	864
	Gly Ser Phe Leu Ala Arg Pro Ser Arg Lys Asn Gln Gly Asp Phe Ser	
	275 280 285	
15	CTC TCC GTC AGG GTG GGG GAT CAG GTG ACC CAT ATT CGG ATC CAG AAC	912
	Leu Ser Val Arg Val Gly Asp Gln Val Thr His Ile Arg Ile Gln Asn	
	290 295 300	
20	TCA GGG GAT TTC TAT GAC CTG TAT GGA GGG GAG AAG TTT GCG ACT CTG	960
	Ser Gly Asp Phe Tyr Asp Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu	
	305 310 315 320	
	ACA GAG CTG GTG GAG TAC TAC ACT CAG CAG CAG GGT GTC CTG CAG GAC	1008
	Thr Glu Leu Val Glu Tyr Tyr Thr Gln Gln Gln Gly Val Leu Gln Asp	
	325 330 335	
25	CGC GAC GGC ACC ATC ATC CAC CTC AAG TAC CCG CTG AAC TGC TCC GAT	1056
	Arg Asp Gly Thr Ile Ile His Leu Lys Tyr Pro Leu Asn Cys Ser Asp	
	340 345 350	
30	CCC ACT AGT GAG AGG TGG TAC CAT GGC CAC ATG TCT GGC GGG CAG GCA	1104
	Pro Thr Ser Glu Arg Trp Tyr His Gly His Met Ser Gly Gly Gln Ala	
	355 360 365	
35	GAG ACG CTG CTG CAG GCC AAG GGC GAG CCC TGG ACG TTT CTT GTG CGT	1152
	Glu Thr Leu Leu Gln Ala Lys Gly Glu Pro Trp Thr Phe Leu Val Arg	
	370 375 380	
40	GAG AGC CTC AGC CAG CCT GGA GAC TTC GTG CTT TCT GTG CTC AGT GAC	1200
	Glu Ser Leu Ser Gln Pro Gly Asp Phe Val Leu Ser Val Leu Ser Asp	
	385 390 395 400	
	CAG CCC AAG GCT GGC CCA GGC TCC CCG CTC AGG GTC ACC CAC ATC AAG	1248
	Gln Pro Lys Ala Gly Pro Gly Ser Pro Leu Arg Val Thr His Ile Lys	
	405 410 415	
45	GTC ATG TGC GAG GGT GGA CGC TAC ACA GTG GGT GGT TTG GAG ACC TTC	1296
	Val Met Cys Glu Gly Gly Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe	
	420 425 430	
50	GAC AGC CTC ACG GAC CTG GTA GAG CAT TTC AAG AAG ACG GGG ATT GAG	1344
	Asp Ser Leu Thr Asp Leu Val Glu His Phe Lys Lys Thr Gly Ile Glu	
	435 440 445	
55	GAG GCC TCA GGC GCC TTT GTC TAC CTG CGG CAG CCG TAC TAT GCC ACG	1392
	Glu Ala Ser Gly Ala Phe Val Tyr Leu Arg Gln Pro Tyr Tyr Ala Thr	
	450 455 460	

215

216

5	AGG GTG AAT GCG GCT GAC ATT GAG AAC CGA GTG TTG GAA CTG AAC AAG	1440
	Arg Val Asn Ala Ala Asp Ile Glu Asn Arg Val Leu Glu Leu Asn Lys	
	465 470 475 480	
10	AAG CAG GAG TCC GAG GAT ACA GCC AAG GCT GGC TTC TGG GAG GAG TTT	1488
	Lys Gln Glu Ser Glu Asp Thr Ala Lys Ala Gly Phe Trp Glu Glu Phe	
	485 490 495	
15	GAG AGT TTG CAG AAG CAG GAG GTG AAG AAC TTG CAC CAG CGT CTG GAA	1536
	Glu Ser Leu Gln Lys Gln Glu Val Lys Asn Leu His Gln Arg Leu Glu	
	500 505 510	
20	GGG CAG CGG CCA GAG AAC AAG GGC AAG AAC CGC TAC AAG AAC ATT CTC	1584
	Gly Gln Arg Pro Glu Asn Lys Gly Lys Asn Arg Tyr Lys Asn Ile Leu	
	515 520 525	
25	CCC TTT GAC CAC AGC CGA GTG ATC CTG CAG GGA CGG GAC AGT AAC ATC	1632
	Pro Phe Asp His Ser Arg Val Ile Leu Gln Gly Arg Asp Ser Asn Ile	
	530 535 540	
30	CCC GGG TCC GAC TAC ATC AAT GCC AAC TAC ATC AAG AAC CAG CTG CTA	1680
	Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile Lys Asn Gln Leu Leu	
	545 550 555 560	
35	GGC CCT GAT GAG AAC GCT AAG ACC TAC ATC GCC AGC CAG GGC TGT CTG	1728
	Gly Pro Asp Glu Asn Ala Lys Thr Tyr Ile Ala Ser Gln Gly Cys Leu	
	565 570 575	
40	GAG GCC ACG GTC AAT GAC TTC TGG CAG ATG GCG TGG CAG GAG AAC AGC	1776
	Glu Ala Thr Val Asn Asp Phe Trp Gln Met Ala Trp Gln Glu Asn Ser	
	580 585 590	
45	CGT GTC ATC GTC ATG ACC ACC CGA GAG GTG GAG AAA GGC CGG AAC AAA	1824
	Arg Val Ile Val Met Thr Thr Arg Glu Val Glu Lys Gly Arg Asn Lys	
	595 600 605	
50	TGC GTC CCA TAC TGG CCC GAG GTG GGC ATG CAG CGT GCT TAT GGG CCC	1872
	Cys Val Pro Tyr Trp Pro Glu Val Gly Met Gln Arg Ala Tyr Gly Pro	
	610 615 620	
55	TAC TCT GTG ACC AAC TGC GGG GAG CAT GAC ACA ACC GAA TAC AAA CTC	1920
	Tyr Ser Val Thr Asn Cys Gly Glu His Asp Thr Thr Glu Tyr Lys Leu	
	625 630 635 640	
60	CGT ACC TTA CAG GTC TCC CCG CTG GAC AAT GGA GAC CTG ATT CGG GAG	1968
	Arg Thr Leu Gln Val Ser Pro Leu Asp Asn Gly Asp Leu Ile Arg Glu	
	645 650 655	
65	ATC TGG CAT TAC CAG TAC CTG AGC TGG CCC GAC CAT GGG GTC CCC AGT	2016
	Ile Trp His Tyr Gln Tyr Leu Ser Trp Pro Asp His Gly Val Pro Ser	
	660 665 670	
70	GAG CCT GGG GGT GTC CTC AGC TTC CTG GAC CAG ATC AAC CAG CGG CAG	2064
	Glu Pro Gly Gly Val Leu Ser Phe Leu Asp Gln Ile Asn Gln Arg Gln	
	675 680 685	

216

217

	GAA AGT CTG CCT CAC GCA GGG CCC ATC ATC GTG CAC TGC AGC GCC GGC	2112
	Glu Ser Leu Pro His Ala Gly Pro Ile Ile Val His Cys Ser Ala Gly	
	690 695 700	
5	ATC GGC CGC ACA GGC ACC ATC ATT GTC ATC GAC ATG CTC ATG GAG AAC	2160
	Ile Gly Arg Thr Gly Thr Ile Ile Val Ile Asp Met Leu Met Glu Asn	
	705 710 715 720	
10	ATC TCC ACC AAG GGC CTG GAC TGT GAC ATT GAC ATC CAG AAG ACC ATC	2208
	Ile Ser Thr Lys Gly Leu Asp Cys Asp Ile Asp Ile Gln Lys Thr Ile	
	725 730 735	
15	CAG ATG GTG CGG GCG CAG CGC TCG GGC ATG GTG CAG ACG GAG GCG CAG	2256
	Gln Met Val Arg Ala Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln	
	740 745 750	
20	TAC AAG TTC ATC TAC GTG GCC ATC GCC CAG TTC ATT GAA ACC ACT AAG	2304
	Tyr Lys Phe Ile Tyr Val Ala Ile Ala Gln Phe Ile Glu Thr Thr Lys	
	755 760 765	
25	AAG AAG CTG GAG GTC CTG CAG TCG CAG AAG GGC CAG GAG TCG GAG TAC	2352
	Lys Lys Leu Glu Val Leu Gln Ser Gln Lys Gly Gln Glu Ser Glu Tyr	
	770 775 780	
30	GGG AAC ATC ACC TAT CCC CCA GCC ATG AAG AAT GCC CAT GCC AAG GCC	2400
	Gly Asn Ile Thr Tyr Pro Pro Ala Met Lys Asn Ala His Ala Lys Ala	
	785 790 795 800	
35	TCC CGC ACC TCG TCC AAA CAC AAG GAG GAT GTG TAT GAG AAC CTG CAC	2448
	Ser Arg Thr Ser Ser Lys His Lys Glu Asp Val Tyr Glu Asn Leu His	
	805 810 815	
40	ACT AAG AAC AAG AGG GAG GAG AAA GTG AAG AAG CAG CGG TCA GCA GAC	2496
	Thr Lys Asn Lys Arg Glu Glu Lys Val Lys Lys Gln Arg Ser Ala Asp	
	820 825 830	
45	AAG GAG AAG AGC AAG GGT TCC CTC AAG AGG AAG TGA	2532
	Lys Glu Lys Ser Lys Gly Ser Leu Lys Arg Lys	
	835 840	

## (2) INFORMATION FOR SEQ ID NO:117:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 843 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- 50 (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

217

218

1 5 10 15  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 5 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 10 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 15 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
 20 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190  
 25 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
 195 200 205  
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220  
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser  
 225 230 235 240  
 30 Gly Leu Arg Ser Arg Glu Met Leu Ser Arg Gly Trp Phe His Arg Asp  
 245 250 255  
 Leu Ser Gly Leu Asp Ala Glu Thr Leu Leu Lys Gly Arg Gly Val His  
 260 265 270  
 35 Gly Ser Phe Leu Ala Arg Pro Ser Arg Lys Asn Gln Gly Asp Phe Ser  
 275 280 285  
 Leu Ser Val Arg Val Gly Asp Gln Val Thr His Ile Arg Ile Gln Asn  
 290 295 300  
 Ser Gly Asp Phe Tyr Asp Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu  
 305 310 315 320  
 40 Thr Glu Leu Val Glu Tyr Tyr Thr Gln Gln Gln Gly Val Leu Gln Asp  
 325 330 335  
 Arg Asp Gly Thr Ile Ile His Leu Lys Tyr Pro Leu Asn Cys Ser Asp  
 340 345 350  
 45 Pro Thr Ser Glu Arg Trp Tyr His Gly His Met Ser Gly Gly Gln Ala  
 355 360 365  
 Glu Thr Leu Leu Gln Ala Lys Gly Glu Pro Trp Thr Phe Leu Val Arg  
 370 375 380  
 Glu Ser Leu Ser Gln Pro Gly Asp Phe Val Leu Ser Val Leu Ser Asp  
 385 390 395 400  
 50 Gln Pro Lys Ala Gly Pro Gly Ser Pro Leu Arg Val Thr His Ile Lys  
 405 410 415  
 Val Met Cys Glu Gly Gly Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe  
 420 425 430  
 Asp Ser Leu Thr Asp Leu Val Glu His Phe Lys Lys Thr Gly Ile Glu  
 435 440 445  
 55 Glu Ala Ser Gly Ala Phe Val Tyr Leu Arg Gln Pro Tyr Tyr Ala Thr

218

219

450                      455                      460  
 Arg Val Asn Ala Ala Asp Ile Glu Asn Arg Val Leu Glu Leu Asn Lys  
 465                      470                      475                      480  
 Lys Gln Glu Ser Glu Asp Thr Ala Lys Ala Gly Phe Trp Glu Glu Phe  
 5                      485                      490                      495  
 Glu Ser Leu Gln Lys Gln Glu Val Lys Asn Leu His Gln Arg Leu Glu  
 500                      505                      510  
 Gly Gln Arg Pro Glu Asn Lys Gly Lys Asn Arg Tyr Lys Asn Ile Leu  
 515                      520                      525  
 10 Pro Phe Asp His Ser Arg Val Ile Leu Gln Gly Arg Asp Ser Asn Ile  
 530                      535                      540  
 Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile Lys Asn Gln Leu Leu  
 545                      550                      555                      560  
 Gly Pro Asp Glu Asn Ala Lys Thr Tyr Ile Ala Ser Gln Gly Cys Leu  
 15                      565                      570                      575  
 Glu Ala Thr Val Asn Asp Phe Trp Gln Met Ala Trp Gln Glu Asn Ser  
 580                      585                      590  
 Arg Val Ile Val Met Thr Thr Arg Glu Val Glu Lys Gly Arg Asn Lys  
 595                      600                      605  
 20 Cys Val Pro Tyr Trp Pro Glu Val Gly Met Gln Arg Ala Tyr Gly Pro  
 610                      615                      620  
 Tyr Ser Val Thr Asn Cys Gly Glu His Asp Thr Thr Glu Tyr Lys Leu  
 625                      630                      635                      640  
 Arg Thr Leu Gln Val Ser Pro Leu Asp Asn Gly Asp Leu Ile Arg Glu  
 25                      645                      650                      655  
 Ile Trp His Tyr Gln Tyr Leu Ser Trp Pro Asp His Gly Val Pro Ser  
 660                      665                      670  
 Glu Pro Gly Gly Val Leu Ser Phe Leu Asp Gln Ile Asn Gln Arg Gln  
 675                      680                      685  
 30 Glu Ser Leu Pro His Ala Gly Pro Ile Ile Val His Cys Ser Ala Gly  
 690                      695                      700  
 Ile Gly Arg Thr Gly Thr Ile Ile Val Ile Asp Met Leu Met Glu Asn  
 705                      710                      715                      720  
 Ile Ser Thr Lys Gly Leu Asp Cys Asp Ile Asp Ile Gln Lys Thr Ile  
 35                      725                      730                      735  
 Gln Met Val Arg Ala Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln  
 740                      745                      750  
 Tyr Lys Phe Ile Tyr Val Ala Ile Ala Gln Phe Ile Glu Thr Thr Lys  
 755                      760                      765  
 40 Lys Lys Leu Glu Val Leu Gln Ser Gln Lys Gly Gln Glu Ser Glu Tyr  
 770                      775                      780  
 Gly Asn Ile Thr Tyr Pro Pro Ala Met Lys Asn Ala His Ala Lys Ala  
 785                      790                      795                      800  
 Ser Arg Thr Ser Ser Lys His Lys Glu Asp Val Tyr Glu Asn Leu His  
 45                      805                      810                      815  
 Thr Lys Asn Lys Arg Glu Glu Lys Val Lys Lys Gln Arg Ser Ala Asp  
 820                      825                      830  
 Lys Glu Lys Ser Lys Gly Ser Leu Lys Arg Lys  
 835                      840

50

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 2562 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

219

220

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

5

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2559

(D) OTHER INFORMATION:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ATG CTG TCC CGT GGG TGG TTT CAC CGA GAC CTC AGT GGG CTG GAT GCA	48
Met Leu Ser Arg Gly Trp Phe His Arg Asp Leu Ser Gly Leu Asp Ala	
1 5 10 15	
GAG ACC CTG CTC AAG GGC CGA GGT GTC CAC GGT AGC TTC CTG GCT CGG	96
Glu Thr Leu Leu Lys Gly Arg Gly Val His Gly Ser Phe Leu Ala Arg	
20 25 30	
CCC AGT CGC AAG AAC CAG GGT GAC TTC TCG CTC TCC GTC AGG GTG GGG	144
Pro Ser Arg Lys Asn Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly	
35 40 45	
GAT CAG GTG ACC CAT ATT CGG ATC CAG AAC TCA GGG GAT TTC TAT GAC	192
Asp Gln Val Thr His Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp	
50 55 60	
CTG TAT GGA GGG GAG AAG TTT GCG ACT CTG ACA GAG CTG GTG GAG TAC	240
Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr	
65 70 75 80	
TAC ACT CAG CAG CAG GGT GTC CTG CAG GAC CGC GAC GGC ACC ATC ATC	288
Tyr Thr Gln Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile	
85 90 95	
CAC CTC AAG TAC CCG CTG AAC TGC TCC GAT CCC ACT AGT GAG AGG TGG	336
His Leu Lys Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp	
100 105 110	
TAC CAT GGC CAC ATG TCT GGC GGG CAG GCA GAG ACG CTG CTG CAG GCC	384
Tyr His Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala	
115 120 125	
AAG GGC GAG CCC TGG ACG TTT CTT GTG CGT GAG AGC CTC AGC CAG CCT	432
Lys Gly Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro	
130 135 140	
GGA GAC TTC GTG CTT TCT GTG CTC AGT GAC CAG CCC AAG GCT GGC CCA	480
Gly Asp Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro	
145 150 155 160	
GGC TCC CCG CTC AGG GTC ACC CAC ATC AAG GTC ATG TGC GAG GGT GGA	528
Gly Ser Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly	
165 170 175	
CGC TAC ACA GTG GGT GGT TTG GAG ACC TTC GAC AGC CTC ACG GAC CTG	576

220



221

	Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu	
	180 185 190	
5	GTA GAG CAT TTC AAG AAG ACG GGG ATT GAG GAG GCC TCA GGC GCC TTT Val Glu His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala Phe	624
	195 200 205	
10	GTC TAC CTG CGG CAG CCG TAC TAT GCC ACG AGG GTG AAT GCG GCT GAC Val Tyr Leu Arg Gln Pro Tyr Tyr Ala Thr Arg Val Asn Ala Ala Asp	672
	210 215 220	
15	ATT GAG AAC CGA GTG TTG GAA CTG AAC AAG AAG CAG GAG TCC GAG GAT Ile Glu Asn Arg Val Leu Glu Leu Asn Lys Lys Gln Glu Ser Glu Asp	720
	225 230 235 240	
	ACA GCC AAG GCT GGC TTC TGG GAG GAG TTT GAG AGT TTG CAG AAG CAG Thr Ala Lys Ala Gly Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln	768
	245 250 255	
20	GAG GTG AAG AAC TTG CAC CAG CGT CTG GAA GGG CAG CGG CCA GAG AAC Glu Val Lys Asn Leu His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn	816
	260 265 270	
25	AAG GGC AAG AAC CGC TAC AAG AAC ATT CTC CCC TTT GAC CAC AGC CGA Lys Gly Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg	864
	275 280 285	
30	GTG ATC CTG CAG GGA CGG GAC AGT AAC ATC CCC GGG TCC GAC TAC ATC Val Ile Leu Gln Gly Arg Asp Ser Asn Ile Pro Gly Ser Asp Tyr Ile	912
	290 295 300	
35	AAT GCC AAC TAC ATC AAG AAC CAG CTG CTA GGC CCT GAT GAG AAC GCT Asn Ala Asn Tyr Ile Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala	960
	305 310 315 320	
	AAG ACC TAC ATC GCC AGC CAG GGC TGT CTG GAG GCC ACG GTC AAT GAC Lys Thr Tyr Ile Ala Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp	1008
	325 330 335	
40	TTC TGG CAG ATG GCG TGG CAG GAG AAC AGC CGT GTC ATC GTC ATG ACC Phe Trp Gln Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr	1056
	340 345 350	
45	ACC CGA GAG GTG GAG AAA GGC CGG AAC AAA TGC GTC CCA TAC TGG CCC Thr Arg Glu Val Glu Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro	1104
	355 360 365	
50	GAG GTG GGC ATG CAG CGT GCT TAT GGG CCC TAC TCT GTG ACC AAC TGC Glu Val Gly Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys	1152
	370 375 380	
55	GGG GAG CAT GAC ACA ACC GAA TAC AAA CTC CGT ACC TTA CAG GTC TCC Gly Glu His Asp Thr Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser	1200
	385 390 395 400	
	CCG CTG GAC AAT GGA GAC CTG ATT CGG GAG ATC TGG CAT TAC CAG TAC	1248

221

222

	Pro	Leu	Asp	Asn	Gly	Asp	Leu	Ile	Arg	Glu	Ile	Trp	His	Tyr	Gln	Tyr	
					405					410					415		
5	CTG	AGC	TGG	CCC	GAC	CAT	GGG	GTC	CCC	AGT	GAG	CCT	GGG	GGT	GTC	CTC	1296
	Leu	Ser	Trp	Pro	Asp	His	Gly	Val	Pro	Ser	Glu	Pro	Gly	Gly	Val	Leu	
				420					425					430			
10	AGC	TTC	CTG	GAC	CAG	ATC	AAC	CAG	CGG	CAG	GAA	AGT	CTG	CCT	CAC	GCA	1344
	Ser	Phe	Leu	Asp	Gln	Ile	Asn	Gln	Arg	Gln	Glu	Ser	Leu	Pro	His	Ala	
			435					440					445				
15	GGG	CCC	ATC	ATC	GTG	CAC	TGC	AGC	GCC	GGC	ATC	GGC	CGC	ACA	GGC	ACC	1392
	Gly	Pro	Ile	Ile	Val	His	Cys	Ser	Ala	Gly	Ile	Gly	Arg	Thr	Gly	Thr	
		450					455					460					
	ATC	ATT	GTC	ATC	GAC	ATG	CTC	ATG	GAG	AAC	ATC	TCC	ACC	AAG	GGC	CTG	1440
	Ile	Ile	Val	Ile	Asp	Met	Leu	Met	Glu	Asn	Ile	Ser	Thr	Lys	Gly	Leu	
	465					470				475					480		
20	GAC	TGT	GAC	ATT	GAC	ATC	CAG	AAG	ACC	ATC	CAG	ATG	GTG	CGG	GCG	CAG	1488
	Asp	Cys	Asp	Ile	Asp	Ile	Gln	Lys	Thr	Ile	Gln	Met	Val	Arg	Ala	Gln	
					485					490				495			
25	CGC	TCG	GGC	ATG	GTG	CAG	ACG	GAG	GCG	CAG	TAC	AAG	TTC	ATC	TAC	GTG	1536
	Arg	Ser	Gly	Met	Val	Gln	Thr	Glu	Ala	Gln	Tyr	Lys	Phe	Ile	Tyr	Val	
			500						505					510			
30	GCC	ATC	GCC	CAG	TTC	ATT	GAA	ACC	ACT	AAG	AAG	AAG	CTG	GAG	GTC	CTG	1584
	Ala	Ile	Ala	Gln	Phe	Ile	Glu	Thr	Thr	Lys	Lys	Lys	Leu	Glu	Val	Leu	
		515						520					525				
35	CAG	TCG	CAG	AAG	GGC	CAG	GAG	TCG	GAG	TAC	GGG	AAC	ATC	ACC	TAT	CCC	1632
	Gln	Ser	Gln	Lys	Gly	Gln	Glu	Ser	Glu	Tyr	Gly	Asn	Ile	Thr	Tyr	Pro	
		530					535					540					
	CCA	GCC	ATG	AAG	AAT	GCC	CAT	GCC	AAG	GCC	TCC	CGC	ACC	TCG	TCC	AAA	1680
	Pro	Ala	Met	Lys	Asn	Ala	His	Ala	Lys	Ala	Ser	Arg	Thr	Ser	Ser	Lys	
	545				550					555					560		
40	CAC	AAG	GAG	GAT	GTG	TAT	GAG	AAC	CTG	CAC	ACT	AAG	AAC	AAG	AGG	GAG	1728
	His	Lys	Glu	Asp	Val	Tyr	Glu	Asn	Leu	His	Thr	Lys	Asn	Lys	Arg	Glu	
					565				570					575			
45	GAG	AAA	GTG	AAG	AAG	CAG	CGG	TCA	GCA	GAC	AAG	GAG	AAG	AGC	AAG	GGT	1776
	Glu	Lys	Val	Lys	Lys	Gln	Arg	Ser	Ala	Asp	Lys	Glu	Lys	Ser	Lys	Gly	
			580						585				590				
50	TCC	CTC	AAG	AGG	AAG	CGA	ATT	CTG	CAG	TCG	ACG	GTA	CCG	CGG	GCC	CGG	1824
	Ser	Leu	Lys	Arg	Lys	Arg	Ile	Leu	Gln	Ser	Thr	Val	Pro	Arg	Ala	Arg	
			595					600					605				
55	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	1872
	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	
		610					615					620					
	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	1920

222

223

	Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His	
	625 630 635 640	
5	AAG TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys	1968
	645 650 655	
10	CTG ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp	2016
	660 665 670	
15	CCC ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg	2064
	675 680 685	
20	TAC CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro	2112
	690 695 700	
25	GAA GGC TAC GTC CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn	2160
	705 710 715 720	
30	TAC AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn	2208
	725 730 735	
35	CGC ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu	2256
	740 745 750	
40	GGG CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met	2304
	755 760 765	
45	GCC GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His	2352
	770 775 780	
50	AAC ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn	2400
	785 790 795 800	
55	ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu	2448
	805 810 815	
60	AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His	2496
	820 825 830	
65	ATG GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met	2544
	835 840 845	
70	GAC GAG CTG TAC AAG TAA	2562

223

224

Asp Glu Leu Tyr Lys  
850

5 (2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 853 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Met Leu Ser Arg Gly Trp Phe His Arg Asp Leu Ser Gly Leu Asp Ala  
1 5 10 15  
20 Glu Thr Leu Leu Lys Gly Arg Gly Val His Gly Ser Phe Leu Ala Arg  
20 25 30  
Pro Ser Arg Lys Asn Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly  
35 40 45  
25 Asp Gln Val Thr His Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp  
50 55 60  
Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr  
65 70 75 80  
Tyr Thr Gln Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile  
85 90 95  
30 His Leu Lys Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp  
100 105 110  
Tyr His Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala  
115 120 125  
35 Lys Gly Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro  
130 135 140  
Gly Asp Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro  
145 150 155 160  
Gly Ser Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly  
165 170 175  
40 Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu  
180 185 190  
Val Glu His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala Phe  
195 200 205  
45 Val Tyr Leu Arg Gln Pro Tyr Tyr Ala Thr Arg Val Asn Ala Ala Asp  
210 215 220  
Ile Glu Asn Arg Val Leu Glu Leu Asn Lys Lys Gln Glu Ser Glu Asp  
225 230 235 240  
Thr Ala Lys Ala Gly Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln  
245 250 255  
50 Glu Val Lys Asn Leu His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn  
260 265 270  
Lys Gly Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg  
275 280 285  
Val Ile Leu Gln Gly Arg Asp Ser Asn Ile Pro Gly Ser Asp Tyr Ile  
55 290 295 300  
Asn Ala Asn Tyr Ile Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala

224

225

305                      310                      315                      320  
 Lys Thr Tyr Ile Ala Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp  
                                  325                      330                      335  
 5 Phe Trp Gln Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr  
                                  340                      345                      350  
 Thr Arg Glu Val Glu Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro  
                                  355                      360                      365  
 Glu Val Gly Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys  
                                  370                      375                      380  
 10 Gly Glu His Asp Thr Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser  
                                  385                      390                      395                      400  
 Pro Leu Asp Asn Gly Asp Leu Ile Arg Glu Ile Trp His Tyr Gln Tyr  
                                  405                      410                      415  
 15 Leu Ser Trp Pro Asp His Gly Val Pro Ser Glu Pro Gly Gly Val Leu  
                                  420                      425                      430  
 Ser Phe Leu Asp Gln Ile Asn Gln Arg Gln Glu Ser Leu Pro His Ala  
                                  435                      440                      445  
 Gly Pro Ile Ile Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr  
                                  450                      455                      460  
 20 Ile Ile Val Ile Asp Met Leu Met Glu Asn Ile Ser Thr Lys Gly Leu  
                                  465                      470                      475                      480  
 Asp Cys Asp Ile Asp Ile Gln Lys Thr Ile Gln Met Val Arg Ala Gln  
                                  485                      490                      495  
 25 Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Lys Phe Ile Tyr Val  
                                  500                      505                      510  
 Ala Ile Ala Gln Phe Ile Glu Thr Thr Lys Lys Lys Leu Glu Val Leu  
                                  515                      520                      525  
 Gln Ser Gln Lys Gly Gln Glu Ser Glu Tyr Gly Asn Ile Thr Tyr Pro  
                                  530                      535                      540  
 30 Pro Ala Met Lys Asn Ala His Ala Lys Ala Ser Arg Thr Ser Ser Lys  
                                  545                      550                      555                      560  
 His Lys Glu Asp Val Tyr Glu Asn Leu His Thr Lys Asn Lys Arg Glu  
                                  565                      570                      575  
 35 Glu Lys Val Lys Lys Gln Arg Ser Ala Asp Lys Glu Lys Ser Lys Gly  
                                  580                      585                      590  
 Ser Leu Lys Arg Lys Arg Ile Leu Gln Ser Thr Val Pro Arg Ala Arg  
                                  595                      600                      605  
 Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr  
                                  610                      615                      620  
 40 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His  
                                  625                      630                      635                      640  
 Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys  
                                  645                      650                      655  
 45 Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp  
                                  660                      665                      670  
 Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg  
                                  675                      680                      685  
 Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro  
                                  690                      695                      700  
 50 Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn  
                                  705                      710                      715                      720  
 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn  
                                  725                      730                      735  
 Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu  
                                  740                      745                      750  
 55 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met

225

226

755                      760                      765  
 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His  
 770                      775                      780  
 5 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn  
 785                      790                      795                      800  
 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu  
 805                      810                      815  
 Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His  
 820                      825                      830  
 10 Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met  
 835                      840                      845  
 Asp Glu Leu Tyr Lys  
 850

15 (2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2994 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

25

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2991

(D) OTHER INFORMATION:

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
35	1                      5                      10                      15	
	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20                      25                      30	
40	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35                      40                      45	
45	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50                      55                      60	
50	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65                      70                      75                      80	
	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85                      90                      95	
55	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336

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227

	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
5	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
10	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
			130					135					140				
15	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
			145				150				155				160		
20	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165					170				175				
25	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
30	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195					200					205				
35	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
			210					215					220				
40	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
			225				230				235				240		
45	GGA	CTC	AGA	TCT	CGA	GCT	CAA	GCT	TCG	AAT	TCG	ACC	ATG	GAG	CGG	CCC	768
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Thr	Met	Glu	Arg	Pro	
				245						250				255			
50	CCG	GGG	CTG	CGG	CCG	GGC	GCG	GGC	GGG	CCC	TGG	GAG	ATG	CGG	GAG	CGG	816
	Pro	Gly	Leu	Arg	Pro	Gly	Ala	Gly	Gly	Pro	Trp	Glu	Met	Arg	Glu	Arg	
				260					265					270			
55	CTG	GGC	ACC	GGC	GGC	TTC	GGG	AAC	GTC	TGT	CTG	TAC	CAG	CAT	CGG	GAA	864
	Leu	Gly	Thr	Gly	Gly	Phe	Gly	Asn	Val	Cys	Leu	Tyr	Gln	His	Arg	Glu	
			275					280					285				
60	CTT	GAT	CTC	AAA	ATA	GCA	ATT	AAG	TCT	TGT	CGC	CTA	GAG	CTA	AGT	ACC	912
	Leu	Asp	Leu	Lys	Ile	Ala	Ile	Lys	Ser	Cys	Arg	Leu	Glu	Leu	Ser	Thr	
			290					295				300					
65	AAA	AAC	AGA	GAA	CGA	TGG	TGC	CAT	GAA	ATC	CAG	ATT	ATG	AAG	AAG	TTG	960
	Lys	Asn	Arg	Glu	Arg	Trp	Cys	His	Glu	Ile	Gln	Ile	Met	Lys	Lys	Leu	
			305				310				315				320		
70	AAC	CAT	GCC	AAT	GTT	GTA	AAG	GCC	TGT	GAT	GTT	CCT	GAA	GAA	TTG	AAT	1008

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	Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro Glu Glu Leu Asn	
	325 330 335	
5	ATT TTG ATT CAT GAT GTG CCT CTT CTA GCA ATG GAA TAC TGT TCT GGA Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu Tyr Cys Ser Gly	1056
	340 345 350	
10	GGA GAT CTC CGA AAG CTG CTC AAC AAA CCA GAA AAT TGT TGT GGA CTT Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn Cys Cys Gly Leu	1104
	355 360 365	
15	AAA GAA AGC CAG ATA CTT TCT TTA CTA AGT GAT ATA GGG TCT GGG ATT Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile Gly Ser Gly Ile	1152
	370 375 380	
20	CGA TAT TTG CAT GAA AAC AAA ATT ATA CAT CGA GAT CTA AAA CCT GAA Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp Leu Lys Pro Glu	1200
	385 390 395 400	
25	AAC ATA GTT CTT CAG GAT GTT GGT GGA AAG ATA ATA CAT AAA ATA ATT Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile His Lys Ile Ile	1248
	405 410 415	
30	GAT CTG GGA TAT GCC AAA GAT GTT GAT CAA GGA AGT CTG TGT ACA TCT Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Ser Leu Cys Thr Ser	1296
	420 425 430	
35	TTT GTG GGA ACA CTG CAG TAT CTG GCC CCA GAG CTC TTT GAG AAT AAG Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu Phe Glu Asn Lys	1344
	435 440 445	
40	CCT TAC ACA GCC ACT GTT GAT TAT TGG AGC TTT GGG ACC ATG GTA TTT Pro Tyr Thr Ala Thr Val Asp Tyr Trp Ser Phe Gly Thr Met Val Phe	1392
	450 455 460	
45	GAA TGT ATT GCT GGA TAT AGG CCT TTT TTG CAT CAT CTG CAG CCA TTT Glu Cys Ile Ala Gly Tyr Arg Pro Phe Leu His His Leu Gln Pro Phe	1440
	465 470 475 480	
50	ACC TGG CAT GAG AAG ATT AAG AAG AAG GAT CCA AAG TGT ATA TTT GCA Thr Trp His Glu Lys Ile Lys Lys Lys Asp Pro Lys Cys Ile Phe Ala	1488
	485 490 495	
55	TGT GAA GAG ATG TCA GGA GAA GTT CGG TTT AGT AGC CAT TTA CCT CAA Cys Glu Glu Met Ser Gly Glu Val Arg Phe Ser Ser His Leu Pro Gln	1536
	500 505 510	
60	CCA AAT AGC CTT TGT AGT TTA ATA GTA GAA CCC ATG GAA AAC TGG CTA Pro Asn Ser Leu Cys Ser Leu Ile Val Glu Pro Met Glu Asn Trp Leu	1584
	515 520 525	
65	CAG TTG ATG TTG AAT TGG GAC CCT CAG CAG AGA GGA GGA CCT GTT GAC Gln Leu Met Leu Asn Trp Asp Pro Gln Gln Arg Gly Gly Pro Val Asp	1632
	530 535 540	
70	CTT ACT TTG AAG CAG CCA AGA TGT TTT GTA TTA ATG GAT CAC ATT TTG	1680

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229

	Leu Thr Leu Lys Gln Pro Arg Cys Phe Val Leu Met Asp His Ile Leu	
	545 550 555 560	
5	AAT TTG AAG ATA GTA CAC ATC CTA AAT ATG ACT TCT GCA AAG ATA ATT Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser Ala Lys Ile Ile	1728
	565 570 575	
10	TCT TTT CTG TTA CCA CCT GAT GAA AGT CTT CAT TCA CTA CAG TCT CGT Ser Phe Leu Leu Pro Pro Asp Glu Ser Leu His Ser Leu Gln Ser Arg	1776
	580 585 590	
15	ATT GAG CGT GAA ACT GGA ATA AAT ACT GGT TCT CAA GAA CTT CTT TCA Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln Glu Leu Leu Ser	1824
	595 600 605	
	GAG ACA GGA ATT TCT CTG GAT CCT CGG AAA CCA GCC TCT CAA TGT GTT Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala Ser Gln Cys Val	1872
	610 615 620	
20	CTA GAT GGA GTT AGA GGC TGT GAT AGC TAT ATG GTT TAT TTG TTT GAT Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val Tyr Leu Phe Asp	1920
	625 630 635 640	
25	AAA AGT AAA ACT GTA TAT GAA GGG CCA TTT GCT TCC AGA AGT TTA TCT Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser Arg Ser Leu Ser	1968
	645 650 655	
30	GAT TGT GTA AAT TAT ATT GTA CAG GAC AGC AAA ATA CAG CTT CCA ATT Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile Gln Leu Pro Ile	2016
	660 665 670	
35	ATA CAG CTG CGT AAA GTG TGG GCT GAA GCA GTG CAC TAT GTG TCT GGA Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His Tyr Val Ser Gly	2064
	675 680 685	
	CTA AAA GAA GAC TAT AGC AGG CTC TTT CAG GGA CAA AGG GCA GCA ATG Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln Arg Ala Ala Met	2112
	690 695 700	
40	TTA AGT CTT CTT AGA TAT AAT GCT AAC TTA ACA AAA ATG AAG AAC ACT Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys Met Lys Asn Thr	2160
	705 710 715 720	
45	TTG ATC TCA GCA TCA CAA CAA CTG AAA GCT AAA TTG GAG TTT TTT CAC Leu Ile Ser Ala Ser Gln Gln Leu Lys Ala Lys Leu Glu Phe Phe His	2208
	725 730 735	
50	AAA AGC ATT CAG CTT GAC TTG GAG AGA TAC AGC GAG CAG ATG ACG TAT Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu Gln Met Thr Tyr	2256
	740 745 750	
55	GGG ATA TCT TCA GAA AAA ATG CTA AAA GCA TGG AAA GAA ATG GAA GAA Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys Glu Met Glu Glu	2304
	755 760 765	
	AAG GCC ATC CAC TAT GCT GAG GTT GGT GTC ATT GGA TAC CTG GAG GAT	2352

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	Lys	Ala	Ile	His	Tyr	Ala	Glu	Val	Gly	Val	Ile	Gly	Tyr	Leu	Glu	Asp	
	770						775					780					
5	CAG	ATT	ATG	TCT	TTG	CAT	GCT	GAA	ATC	ATG	GGG	CTA	CAG	AAG	AGC	CCC	2400
	Gln	Ile	Met	Ser	Leu	His	Ala	Glu	Ile	Met	Gly	Leu	Gln	Lys	Ser	Pro	
	785					790					795					800	
10	TAT	GGA	AGA	CGT	CAG	GGA	GAC	TTG	ATG	GAA	TCT	CTG	GAA	CAG	CGT	GCC	2448
	Tyr	Gly	Arg	Arg	Gln	Gly	Asp	Leu	Met	Glu	Ser	Leu	Glu	Gln	Arg	Ala	
				805						810					815		
15	ATT	GAT	CTA	TAT	AAG	CAG	TTA	AAA	CAC	AGA	CCT	TCA	GAT	CAC	TCC	TAC	2496
	Ile	Asp	Leu	Tyr	Lys	Gln	Leu	Lys	His	Arg	Pro	Ser	Asp	His	Ser	Tyr	
				820					825						830		
20	AGT	GAC	AGC	ACA	GAG	ATG	GTG	AAA	ATC	ATT	GTG	CAC	ACT	GTG	CAG	AGT	2544
	Ser	Asp	Ser	Thr	Glu	Met	Val	Lys	Ile	Ile	Val	His	Thr	Val	Gln	Ser	
				835				840					845				
25	CAG	GAC	CGT	GTG	CTC	AAG	GAG	CTG	TTT	GGT	CAT	TTG	AGC	AAG	TTG	TTG	2592
	Gln	Asp	Arg	Val	Leu	Lys	Glu	Leu	Phe	Gly	His	Leu	Ser	Lys	Leu	Leu	
		850					855					860					
30	GGC	TGT	AAG	CAG	AAG	ATT	ATT	GAT	CTA	CTC	CCT	AAG	GTG	GAA	GTG	GCC	2640
	Gly	Cys	Lys	Gln	Lys	Ile	Ile	Asp	Leu	Leu	Pro	Lys	Val	Glu	Val	Ala	
	865					870					875					880	
35	CTC	AGT	AAT	ATC	AAA	GAA	GCT	GAC	AAT	ACT	GTC	ATG	TTC	ATG	CAG	GGA	2688
	Leu	Ser	Asn	Ile	Lys	Glu	Ala	Asp	Asn	Thr	Val	Met	Phe	Met	Gln	Gly	
				885						890					895		
40	AAA	AGG	CAG	AAA	GAA	ATA	TGG	CAT	CTC	CTT	AAA	ATT	GCC	TGT	ACA	CAG	2736
	Lys	Arg	Gln	Lys	Glu	Ile	Trp	His	Leu	Leu	Lys	Ile	Ala	Cys	Thr	Gln	
				900					905					910			
45	AGT	TCT	GCC	CGC	TCT	CTT	GTA	GGA	TCC	AGT	CTA	GAA	GGT	GCA	GTA	ACC	2784
	Ser	Ser	Ala	Arg	Ser	Leu	Val	Gly	Ser	Ser	Leu	Glu	Gly	Ala	Val	Thr	
			915					920					925				
50	CCT	CAG	ACA	TCA	GCA	TGG	CTG	CCC	CCG	ACT	TCA	GCA	GAA	CAT	GAT	CAT	2832
	Pro	Gln	Thr	Ser	Ala	Trp	Leu	Pro	Pro	Thr	Ser	Ala	Glu	His	Asp	His	
		930					935					940					
55	TCT	CTG	TCA	TGT	GTG	GTA	ACT	CCT	CAA	GAT	GGG	GAG	ACT	TCA	GCA	CAA	2880
	Ser	Leu	Ser	Cys	Val	Val	Thr	Pro	Gln	Asp	Gly	Glu	Thr	Ser	Ala	Gln	
	945					950					955					960	
60	ATG	ATA	GAA	GAA	AAT	TTG	AAC	TGC	CTT	GGC	CAT	TTA	AGC	ACT	ATT	ATT	2928
	Met	Ile	Glu	Glu	Asn	Leu	Asn	Cys	Leu	Gly	His	Leu	Ser	Thr	Ile	Ile	
					965					970					975		
65	CAT	GAG	GCA	AAT	GAG	GAA	CAG	GGC	AAT	AGT	ATG	ATG	AAT	CTT	GAT	TGG	2976
	His	Glu	Ala	Asn	Glu	Glu	Gln	Gly	Asn	Ser	Met	Met	Asn	Leu	Asp	Trp	
				980					985					990			
70	AGT	TGG	TTA	ACA	GAA	TGA											2994
																	230

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Ser Trp Leu Thr Glu  
995

5 (2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 997 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10					15		
20	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
				35					40					45			
25	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
		50				55						60					
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65				70					75					80		
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85						90					95		
30	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
35			130				135						140				
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145				150						155				160		
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165					170					175			
40	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195				200						205				
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
45			210				215						220				
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225				230						235				240		
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Thr	Met	Glu	Arg	Pro	
				245					250					255			
50	Pro	Gly	Leu	Arg	Pro	Gly	Ala	Gly	Gly	Pro	Trp	Glu	Met	Arg	Glu	Arg	
				260				265						270			
	Leu	Gly	Thr	Gly	Gly	Phe	Gly	Asn	Val	Cys	Leu	Tyr	Gln	His	Arg	Glu	
			275				280						285				
	Leu	Asp	Leu	Lys	Ile	Ala	Ile	Lys	Ser	Cys	Arg	Leu	Glu	Leu	Ser	Thr	
55			290				295					300					
	Lys	Asn	Arg	Glu	Arg	Trp	Cys	His	Glu	Ile	Gln	Ile	Met	Lys	Lys	Leu	

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SUBSTITUTE SHEET (RULE 26)

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	305					310				315						320
	Asn	His	Ala	Asn	Val	Val	Lys	Ala	Cys	Asp	Val	Pro	Glu	Glu	Leu	Asn
					325					330						335
5	Ile	Leu	Ile	His	Asp	Val	Pro	Leu	Leu	Ala	Met	Glu	Tyr	Cys	Ser	Gly
				340					345					350		
	Gly	Asp	Leu	Arg	Lys	Leu	Leu	Asn	Lys	Pro	Glu	Asn	Cys	Cys	Gly	Leu
			355					360				365				
	Lys	Glu	Ser	Gln	Ile	Leu	Ser	Leu	Leu	Ser	Asp	Ile	Gly	Ser	Gly	Ile
			370				375					380				
10	Arg	Tyr	Leu	His	Glu	Asn	Lys	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Glu
	385					390					395					400
	Asn	Ile	Val	Leu	Gln	Asp	Val	Gly	Gly	Lys	Ile	Ile	His	Lys	Ile	Ile
				405						410					415	
15	Asp	Leu	Gly	Tyr	Ala	Lys	Asp	Val	Asp	Gln	Gly	Ser	Leu	Cys	Thr	Ser
			420						425					430		
	Phe	Val	Gly	Thr	Leu	Gln	Tyr	Leu	Ala	Pro	Glu	Leu	Phe	Glu	Asn	Lys
			435					440					445			
	Pro	Tyr	Thr	Ala	Thr	Val	Asp	Tyr	Trp	Ser	Phe	Gly	Thr	Met	Val	Phe
			450				455					460				
20	Glu	Cys	Ile	Ala	Gly	Tyr	Arg	Pro	Phe	Leu	His	His	Leu	Gln	Pro	Phe
	465					470					475					480
	Thr	Trp	His	Glu	Lys	Ile	Lys	Lys	Lys	Asp	Pro	Lys	Cys	Ile	Phe	Ala
				485						490					495	
25	Cys	Glu	Glu	Met	Ser	Gly	Glu	Val	Arg	Phe	Ser	Ser	His	Leu	Pro	Gln
			500						505				510			
	Pro	Asn	Ser	Leu	Cys	Ser	Leu	Ile	Val	Glu	Pro	Met	Glu	Asn	Trp	Leu
			515					520					525			
	Gln	Leu	Met	Leu	Asn	Trp	Asp	Pro	Gln	Gln	Arg	Gly	Gly	Pro	Val	Asp
			530				535					540				
30	Leu	Thr	Leu	Lys	Gln	Pro	Arg	Cys	Phe	Val	Leu	Met	Asp	His	Ile	Leu
	545					550					555					560
	Asn	Leu	Lys	Ile	Val	His	Ile	Leu	Asn	Met	Thr	Ser	Ala	Lys	Ile	Ile
				565						570					575	
35	Ser	Phe	Leu	Leu	Pro	Pro	Asp	Glu	Ser	Leu	His	Ser	Leu	Gln	Ser	Arg
			580						585					590		
	Ile	Glu	Arg	Glu	Thr	Gly	Ile	Asn	Thr	Gly	Ser	Gln	Glu	Leu	Leu	Ser
			595					600					605			
	Glu	Thr	Gly	Ile	Ser	Leu	Asp	Pro	Arg	Lys	Pro	Ala	Ser	Gln	Cys	Val
			610				615					620				
40	Leu	Asp	Gly	Val	Arg	Gly	Cys	Asp	Ser	Tyr	Met	Val	Tyr	Leu	Phe	Asp
	625					630					635					640
	Lys	Ser	Lys	Thr												

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755 760 765  
 Lys Ala Ile His Tyr Ala Glu Val Gly Val Ile Gly Tyr Leu Glu Asp  
 770 775 780  
 5 Gln Ile Met Ser Leu His Ala Glu Ile Met Gly Leu Gln Lys Ser Pro  
 785 790 795 800  
 Tyr Gly Arg Arg Gln Gly Asp Leu Met Glu Ser Leu Glu Gln Arg Ala  
 805 810 815  
 Ile Asp Leu Tyr Lys Gln Leu Lys His Arg Pro Ser Asp His Ser Tyr  
 820 825 830  
 10 Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His Thr Val Gln Ser  
 835 840 845  
 Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu Ser Lys Leu Leu  
 850 855 860  
 15 Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys Val Glu Val Ala  
 865 870 875 880  
 Leu Ser Asn Ile Lys Glu Ala Asp Asn Thr Val Met Phe Met Gln Gly  
 885 890 895  
 Lys Arg Gln Lys Glu Ile Trp His Leu Leu Lys Ile Ala Cys Thr Gln  
 900 905 910  
 20 Ser Ser Ala Arg Ser Leu Val Gly Ser Ser Leu Glu Gly Ala Val Thr  
 915 920 925  
 Pro Gln Thr Ser Ala Trp Leu Pro Pro Thr Ser Ala Glu His Asp His  
 930 935 940  
 25 Ser Leu Ser Cys Val Val Thr Pro Gln Asp Gly Glu Thr Ser Ala Gln  
 945 950 955 960  
 Met Ile Glu Glu Asn Leu Asn Cys Leu Gly His Leu Ser Thr Ile Ile  
 965 970 975  
 His Glu Ala Asn Glu Glu Gln Gly Asn Ser Met Met Asn Leu Asp Trp  
 980 985 990  
 30 Ser Trp Leu Thr Glu  
 995

## (2) INFORMATION FOR SEQ ID NO:122:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2991 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 40  
 (ii) MOLECULE TYPE: cDNA  
 (ix) FEATURE:  
 (A) NAME/KEY: Coding Sequence  
 45 (B) LOCATION: 1...2988  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

50 ATG GAG CGG CCC CCG GGG CTG CGG CCG GGC GCG GGC GGG CCC TGG GAG 48  
 Met Glu Arg Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu  
 1 5 10 15  
 55 ATG CGG GAG CGG CTG GGC ACC GGC GGC TTC GGG AAC GTC TGT CTG TAC 96  
 Met Arg Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Cys Leu Tyr  
 20 25 30

233

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5	CAG CAT CGG GAA CTT GAT CTC AAA ATA GCA ATT AAG TCT TGT CGC CTA Gln His Arg Glu Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu 35 40 45	144
	GAG CTA AGT ACC AAA AAC AGA GAA CGA TGG TGC CAT GAA ATC CAG ATT Glu Leu Ser Thr Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile 50 55 60	192
	ATG AAG AAG TTG AAC CAT GCC AAT GTT GTA AAG GCC TGT GAT GTT CCT Met Lys Lys Leu Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro 65 70 75 80	240
	GAA GAA TTG AAT ATT TTG ATT CAT GAT GTG CCT CTT CTA GCA ATG GAA Glu Glu Leu Asn Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu 85 90 95	288
	TAC TGT TCT GGA GGA GAT CTC CGA AAG CTG CTC AAC AAA CCA GAA AAT Tyr Cys Ser Gly Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn 100 105 110	336
20	TGT TGT GGA CTT AAA GAA AGC CAG ATA CTT TCT TTA CTA AGT GAT ATA Cys Cys Gly Leu Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile 115 120 125	384
	GGG TCT GGG ATT CGA TAT TTG CAT GAA AAC AAA ATT ATA CAT CGA GAT Gly Ser Gly Ile Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp 130 135 140	432
	CTA AAA CCT GAA AAC ATA GTT CTT CAG GAT GTT GGT GGA AAG ATA ATA Leu Lys Pro Glu Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile 145 150 155 160	480
	CAT AAA ATA ATT GAT CTG GGA TAT GCC AAA GAT GTT GAT CAA GGA AGT His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Ser 165 170 175	528
	CTG TGT ACA TCT TTT GTG GGA ACA CTG CAG TAT CTG GCC CCA GAG CTC Leu Cys Thr Ser Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu 180 185 190	576
40	TTT GAG AAT AAG CCT TAC ACA GCC ACT GTT GAT TAT TGG AGC TTT GGG Phe Glu Asn Lys Pro Tyr Thr Ala Thr Val Asp Tyr Trp Ser Phe Gly 195 200 205	624
	ACC ATG GTA TTT GAA TGT ATT GCT GGA TAT AGG CCT TTT TTG CAT CAT Thr Met Val Phe Glu Cys Ile Ala Gly Tyr Arg Pro Phe Leu His His 210 215 220	672
	CTG CAG CCA TTT ACC TGG CAT GAG AAG ATT AAG AAG AAG GAT CCA AAG Leu Gln Pro Phe Thr Trp His Glu Lys Ile Lys Lys Lys Asp Pro Lys 225 230 235 240	720
	TGT ATA TTT GCA TGT GAA GAG ATG TCA GGA GAA GTT CGG TTT AGT AGC Cys Ile Phe Ala Cys Glu Glu Met Ser Gly Glu Val Arg Phe Ser Ser 245 250 255	768

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235

	CAT TTA CCT CAA CCA AAT AGC CTT TGT AGT TTA ATA GTA GAA CCC ATG	816
	His Leu Pro Gln Pro Asn Ser Leu Cys Ser Leu Ile Val Glu Pro Met	
	260 265 270	
5	GAA AAC TGG CTA CAG TTG ATG TTG AAT TGG GAC CCT CAG CAG AGA GGA	864
	Glu Asn Trp Leu Gln Leu Met Leu Asn Trp Asp Pro Gln Gln Arg Gly	
	275 280 285	
10	GGA CCT GTT GAC CTT ACT TTG AAG CAG CCA AGA TGT TTT GTA TTA ATG	912
	Gly Pro Val Asp Leu Thr Leu Lys Gln Pro Arg Cys Phe Val Leu Met	
	290 295 300	
15	GAT CAC ATT TTG AAT TTG AAG ATA GTA CAC ATC CTA AAT ATG ACT TCT	960
	Asp His Ile Leu Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser	
	305 310 315 320	
20	GCA AAG ATA ATT TCT TTT CTG TTA CCA CCT GAT GAA AGT CTT CAT TCA	1008
	Ala Lys Ile Ile Ser Phe Leu Leu Pro Pro Asp Glu Ser Leu His Ser	
	325 330 335	
	CTA CAG TCT CGT ATT GAG CGT GAA ACT GGA ATA AAT ACT GGT TCT CAA	1056
	Leu Gln Ser Arg Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln	
	340 345 350	
25	GAA CTT CTT TCA GAG ACA GGA ATT TCT CTG GAT CCT CGG AAA CCA GCC	1104
	Glu Leu Leu Ser Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala	
	355 360 365	
30	TCT CAA TGT GTT CTA GAT GGA GTT AGA GGC TGT GAT AGC TAT ATG GTT	1152
	Ser Gln Cys Val Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val	
	370 375 380	
35	TAT TTG TTT GAT AAA AGT AAA ACT GTA TAT GAA GGG CCA TTT GCT TCC	1200
	Tyr Leu Phe Asp Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser	
	385 390 395 400	
40	AGA AGT TTA TCT GAT TGT GTA AAT TAT ATT GTA CAG GAC AGC AAA ATA	1248
	Arg Ser Leu Ser Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile	
	405 410 415	
	CAG CTT CCA ATT ATA CAG CTG CGT AAA GTG TGG GCT GAA GCA GTG CAC	1296
	Gln Leu Pro Ile Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His	
	420 425 430	
45	TAT GTG TCT GGA CTA AAA GAA GAC TAT AGC AGG CTC TTT CAG GGA CAA	1344
	Tyr Val Ser Gly Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln	
	435 440 445	
50	AGG GCA GCA ATG TTA AGT CTT CTT AGA TAT AAT GCT AAC TTA ACA AAA	1392
	Arg Ala Ala Met Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys	
	450 455 460	
55	ATG AAG AAC ACT TTG ATC TCA GCA TCA CAA CAA CTG AAA GCT AAA TTG	1440
	Met Lys Asn Thr Leu Ile Ser Ala Ser Gln Gln Leu Lys Ala Lys Leu	
	465 470 475 480	

235

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	GAG TTT TTT CAC AAA AGC ATT CAG CTT GAC TTG GAG AGA TAC AGC GAG	1488
	Glu Phe Phe His Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu	
	485 490 495	
5	CAG ATG ACG TAT GGG ATA TCT TCA GAA AAA ATG CTA AAA GCA TGG AAA	1536
	Gln Met Thr Tyr Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys	
	500 505 510	
10	GAA ATG GAA GAA AAG GCC ATC CAC TAT GCT GAG GTT GGT GTC ATT GGA	1584
	Glu Met Glu Glu Lys Ala Ile His Tyr Ala Glu Val Gly Val Ile Gly	
	515 520 525	
15	TAC CTG GAG GAT CAG ATT ATG TCT TTG CAT GCT GAA ATC ATG GGG CTA	1632
	Tyr Leu Glu Asp Gln Ile Met Ser Leu His Ala Glu Ile Met Gly Leu	
	530 535 540	
20	CAG AAG AGC CCC TAT GGA AGA CGT CAG GGA GAC TTG ATG GAA TCT CTG	1680
	Gln Lys Ser Pro Tyr Gly Arg Arg Gln Gly Asp Leu Met Glu Ser Leu	
	545 550 555 560	
	GAA CAG CGT GCC ATT GAT CTA TAT AAG CAG TTA AAA CAC AGA CCT TCA	1728
	Glu Gln Arg Ala Ile Asp Leu Tyr Lys Gln Leu Lys His Arg Pro Ser	
	565 570 575	
25	GAT CAC TCC TAC AGT GAC AGC ACA GAG ATG GTG AAA ATC ATT GTG CAC	1776
	Asp His Ser Tyr Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His	
	580 585 590	
30	ACT GTG CAG AGT CAG GAC CGT GTG CTC AAG GAG CTG TTT GGT CAT TTG	1824
	Thr Val Gln Ser Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu	
	595 600 605	
35	AGC AAG TTG TTG GGC TGT AAG CAG AAG ATT ATT GAT CTA CTC CCT AAG	1872
	Ser Lys Leu Leu Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys	
	610 615 620	
40	GTG GAA GTG GCC CTC AGT AAT ATC AAA GAA GCT GAC AAT ACT GTC ATG	1920
	Val Glu Val Ala Leu Ser Asn Ile Lys Glu Ala Asp Asn Thr Val Met	
	625 630 635 640	
	TTC ATG CAG GGA AAA AGG CAG AAA GAA ATA TGG CAT CTC CTT AAA ATT	1968
	Phe Met Gln Gly Lys Arg Gln Lys Glu Ile Trp His Leu Leu Lys Ile	
	645 650 655	
45	GCC TGT ACA CAG AGT TCT GCC CGC TCT CTT GTA GGA TCC AGT CTA GAA	2016
	Ala Cys Thr Gln Ser Ser Ala Arg Ser Leu Val Gly Ser Ser Leu Glu	
	660 665 670	
50	GGT GCA GTA ACC CCT CAG ACA TCA GCA TGG CTG CCC CCG ACT TCA GCA	2064
	Gly Ala Val Thr Pro Gln Thr Ser Ala Trp Leu Pro Pro Thr Ser Ala	
	675 680 685	
55	GAA CAT GAT CAT TCT CTG TCA TGT GTG GTA ACT CCT CAA GAT GGG GAG	2112
	Glu His Asp His Ser Leu Ser Cys Val Val Thr Pro Gln Asp Gly Glu	
	690 695 700	

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5	ACT TCA GCA CAA ATG ATA GAA GAA AAT TTG AAC TGC CTT GGC CAT TTA	2160
	Thr Ser Ala Gln Met Ile Glu Glu Asn Leu Asn Cys Leu Gly His Leu	
	705 710 715 720	
10	AGC ACT ATT ATT CAT GAG GCA AAT GAG GAA CAG GGC AAT AGT ATG ATG	2208
	Ser Thr Ile Ile His Glu Ala Asn Glu Glu Gln Gly Asn Ser Met Met	
	725 730 735	
15	AAT CTT GAT TGG AGT TGG TTA ACA GAA TGG GTA CCG CGG GCC CGG GAT	2256
	Asn Leu Asp Trp Ser Trp Leu Thr Glu Trp Val Pro Arg Ala Arg Asp	
	740 745 750	
20	CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG	2304
	Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly	
	755 760 765	
25	GTG GTG CCC ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG	2352
	Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys	
	770 775 780	
30	TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG	2400
	Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu	
	785 790 795 800	
35	ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC	2448
	Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro	
	805 810 815	
40	ACC CTC GTG ACC ACC CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC	2496
	Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr	
	820 825 830	
45	CCC GAC CAC ATG AAG CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA	2544
	Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu	
	835 840 845	
50	GGC TAC GTC CAG GAG CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC	2592
	Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr	
	850 855 860	
55	AAG ACC CGC GCC GAG GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC	2640
	Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg	
	865 870 875 880	
60	ATC GAG CTG AAG GGC ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG	2688
	Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly	
	885 890 895	
65	CAC AAG CTG GAG TAC AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC	2736
	His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala	
	900 905 910	
70	GAC AAG CAG AAG AAC GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC	2784
	Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn	
	915 920 925	

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5 ATC GAG GAC GGC AGC GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC 2832  
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr  
 930 935 940  
 CCC ATC GGC GAC GGC CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC 2880  
 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser  
 945 950 955 960  
 10 ACC CAG TCC GCC CTG AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG 2928  
 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met  
 965 970 975  
 15 GTC CTG CTG GAG TTC GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC 2976  
 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp  
 980 985 990  
 GAG CTG TAC AAG TAA 2991  
 Glu Leu Tyr Lys  
 20 995

## (2) INFORMATION FOR SEQ ID NO:123:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 996 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Met Glu Arg Pro Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu  
 1 5 10 15  
 Met Arg Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Cys Leu Tyr  
 20 25 30  
 40 Gln His Arg Glu Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu  
 35 40 45  
 Glu Leu Ser Thr Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile  
 50 55 60  
 Met Lys Lys Leu Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro  
 45 65 70 75 80  
 Glu Glu Leu Asn Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu  
 85 90 95  
 Tyr Cys Ser Gly Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn  
 100 105 110  
 50 Cys Cys Gly Leu Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile  
 115 120 125  
 Gly Ser Gly Ile Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp  
 130 135 140  
 Leu Lys Pro Glu Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile  
 55 145 150 155 160  
 His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Ser

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				165				170				175				
	Leu	Cys	Thr	Ser	Phe	Val	Gly	Thr	Leu	Gln	Tyr	Leu	Ala	Pro	Glu	Leu
				180				185					190			
5	Phe	Glu	Asn	Lys	Pro	Tyr	Thr	Ala	Thr	Val	Asp	Tyr	Trp	Ser	Phe	Gly
			195					200					205			
	Thr	Met	Val	Phe	Glu	Cys	Ile	Ala	Gly	Tyr	Arg	Pro	Phe	Leu	His	His
		210					215					220				
	Leu	Gln	Pro	Phe	Thr	Trp	His	Glu	Lys	Ile	Lys	Lys	Lys	Asp	Pro	Lys
	225						230					235				240
10	Cys	Ile	Phe	Ala	Cys	Glu	Glu	Met	Ser	Gly	Glu	Val	Arg	Phe	Ser	Ser
					245					250					255	
	His	Leu	Pro	Gln	Pro	Asn	Ser	Leu	Cys	Ser	Leu	Ile	Val	Glu	Pro	Met
			260						265					270		
15	Glu	Asn	Trp	Leu	Gln	Leu	Met	Leu	Asn	Trp	Asp	Pro	Gln	Gln	Arg	Gly
		275						280					285			
	Gly	Pro	Val	Asp	Leu	Thr	Leu	Lys	Gln	Pro	Arg	Cys	Phe	Val	Leu	Met
		290					295					300				
	Asp	His	Ile	Leu	Asn	Leu	Lys	Ile	Val	His	Ile	Leu	Asn	Met	Thr	Ser
	305					310					315					320
20	Ala	Lys	Ile	Ile	Ser	Phe	Leu	Leu	Pro	Pro	Asp	Glu	Ser	Leu	His	Ser
					325					330					335	
	Leu	Gln	Ser	Arg	Ile	Glu	Arg	Glu	Thr	Gly	Ile	Asn	Thr	Gly	Ser	Gln
			340					345						350		
25	Glu	Leu	Leu	Ser	Glu	Thr	Gly	Ile	Ser	Leu	Asp	Pro	Arg	Lys	Pro	Ala
		355						360					365			
	Ser	Gln	Cys	Val	Leu	Asp	Gly	Val	Arg	Gly	Cys	Asp	Ser	Tyr	Met	Val
		370					375					380				
	Tyr	Leu	Phe	Asp	Lys	Ser	Lys	Thr	Val	Tyr	Glu	Gly	Pro	Phe	Ala	Ser
	385					390					395					400
30	Arg	Ser	Leu	Ser	Asp	Cys	Val	Asn	Tyr	Ile	Val	Gln	Asp	Ser	Lys	Ile
					405						410				415	
	Gln	Leu	Pro	Ile	Ile	Gln	Leu	Arg	Lys	Val	Trp	Ala	Glu	Ala	Val	His
			420						425					430		
35	Tyr	Val	Ser	Gly	Leu	Lys	Glu	Asp	Tyr	Ser	Arg	Leu	Phe	Gln	Gly	Gln
		435						440					445			
	Arg	Ala	Ala	Met	Leu	Ser	Leu	Leu	Arg	Tyr	Asn	Ala	Asn	Leu	Thr	Lys
		450					455					460				
	Met	Lys	Asn	Thr	Leu	Ile	Ser	Ala	Ser	Gln	Gln	Leu	Lys	Ala	Lys	Leu
	465					470					475					480
40	Glu	Phe	Phe	His	Lys	Ser	Ile	Gln	Leu	Asp	Leu	Glu	Arg	Tyr	Ser	Glu
					485					490					495	
	Gln	Met	Thr	Tyr	Gly	Ile	Ser	Ser	Glu	Lys	Met	Leu	Lys	Ala	Trp	Lys
			500						505						510	
45	Glu	Met	Glu	Glu	Lys	Ala	Ile	His	Tyr	Ala	Glu	Val	Gly	Val	Ile	Gly
		515						520					525			
	Tyr	Leu	Glu	Asp	Gln	Ile	Met	Ser	Leu	His	Ala	Glu	Ile	Met	Gly	Leu
		530					535					540				
	Gln	Lys	Ser	Pro	Tyr	Gly	Arg	Arg	Gln	Gly	Asp	Leu	Met	Glu	Ser	Leu
	545					550					555					560
50	Glu	Gln	Arg	Ala	Ile	Asp	Leu	Tyr	Lys	Gln	Leu	Lys	His	Arg	Pro	Ser
					565					570					575	
	Asp	His	Ser	Tyr	Ser	Asp	Ser	Thr	Glu	Met	Val	Lys	Ile	Ile	Val	His
			580						585					590		
55	Thr	Val	Gln	Ser	Gln	Asp	Arg	Val	Leu	Lys	Glu	Leu	Phe	Gly	His	Leu
			595					600					605			
	Ser	Lys	Leu	Leu	Gly	Cys	Lys	Gln	Lys	Ile	Ile	Asp	Leu	Leu	Pro	Lys

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[illegible]

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1908 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

241

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

5

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1905

(D) OTHER INFORMATION:

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

15	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
15	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
20	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
25	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
30	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
35	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
40	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
40	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
45	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
50	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
55	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
55	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC	576

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	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
5	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195					200					205				
10	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215					220					
15	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
		225				230					235				240		
20	GGA	CTC	AGA	TCT	CGA	GCT	CAA	GCT	TCC	ATG	AGC	GAG	ACG	GTC	ATC	ATG	768
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Met	Ser	Glu	Thr	Val	Ile	Met	
					245					250					255		
25	AGC	GAG	ACG	GTC	ATC	TGT	TCC	AGC	CGG	GCC	ACT	GTG	ATG	CTT	TAT	GAT	816
	Ser	Glu	Thr	Val	Ile	Cys	Ser	Ser	Arg	Ala	Thr	Val	Met	Leu	Tyr	Asp	
			260						265					270			
30	GAT	GGC	AAC	AAG	CGA	TGG	CTC	CCT	GCT	GGC	ACG	GGT	CCC	CAG	GCC	TTC	864
	Asp	Gly	Asn	Lys	Arg	Trp	Leu	Pro	Ala	Gly	Thr	Gly	Pro	Gln	Ala	Phe	
		275						280					285				
35	AGC	CGC	GTC	CAG	ATC	TAC	CAC	AAC	CCC	ACG	GCC	AAT	TCC	TTT	CGC	GTC	912
	Ser	Arg	Val	Gln	Ile	Tyr	His	Asn	Pro	Thr	Ala	Asn	Ser	Phe	Arg	Val	
		290					295					300					
40	GTG	GGC	CGG	AAG	ATG	CAG	CCC	GAC	CAG	CAG	GTG	GTC	ATC	AAC	TGT	GCC	960
	Val	Gly	Arg	Lys	Met	Gln	Pro	Asp	Gln	Gln	Val	Val	Ile	Asn	Cys	Ala	
		305				310					315				320		
45	ATC	GTC	CGG	GGT	GTG	AAG	TAT	AAC	CAG	GCC	ACC	CCC	AAC	TTC	CAT	CAG	1008
	Ile	Val	Arg	Gly	Val	Lys	Tyr	Asn	Gln	Ala	Thr	Pro	Asn	Phe	His	Gln	
					325					330					335		
50	TGG	CGC	GAC	GCT	CGC	CAG	GTC	TGG	GGC	CTC	AAC	TTC	GGC	AGC	AAG	GAG	1056
	Trp	Arg	Asp	Ala	Arg	Gln	Val	Trp	Gly	Leu	Asn	Phe	Gly	Ser	Lys	Glu	
			340						345					350			
55	GAT	GCG	GCC	CAG	TTT	GCC	GCC	GGC	ATG	GCC	AGT	GCC	CTA	GAG	GCG	TTG	1104
	Asp	Ala	Ala	Gln	Phe	Ala	Ala	Gly	Met	Ala	Ser	Ala	Leu	Glu	Ala	Leu	
		355						360					365				
60	GAA	GGA	GGT	GGG	CCC	CCT	CCA	CCC	CCA	GCA	CTT	CCC	ACC	TGG	TCG	GTC	1152
	Glu	Gly	Gly	Gly	Pro	Pro	Pro	Pro	Pro	Ala	Leu	Pro	Thr	Trp	Ser	Val	
		370					375					380					
65	CCG	AAC	GGC	CCC	TCC	CCG	GAG	GAG	GTG	GAG	CAG	CAG	AAA	AGG	CAG	CAG	1200
	Pro	Asn	Gly	Pro	Ser	Pro	Glu	Glu	Val	Glu	Gln	Gln	Lys	Arg	Gln	Gln	
		385				390				395					400		
70	CCC	GGC	CCG	TCG	GAG	CAC	ATA	GAG	CGC	CGG	GTC	TCC	AAT	GCA	GGA	GGC	1248

242

243

	Pro	Gly	Pro	Ser	Glu	His	Ile	Glu	Arg	Arg	Val	Ser	Asn	Ala	Gly	Gly	
					405					410					415		
5	CCA	CCT	GCT	CCC	CCC	GCT	GGG	GGT	CCA	CCC	CCA	CCA	CCA	GGA	CCT	CCC	1296
	Pro	Pro	Ala	Pro	Pro	Ala	Gly	Gly	Pro	Pro	Pro	Pro	Pro	Gly	Pro	Pro	
					420				425					430			
10	CCT	CCT	CCA	GGT	CCC	CCC	CCA	CCC	CCA	GGT	TTG	CCC	CCT	TCG	GGG	GTC	1344
	Pro	Pro	Pro	Gly	Pro	Pro	Pro	Pro	Pro	Gly	Leu	Pro	Pro	Ser	Gly	Val	
				435					440					445			
15	CCA	GCT	GCA	GCG	CAC	GGA	GCA	GGG	GGA	GGA	CCA	CCC	CCT	GCA	CCC	CCT	1392
	Pro	Ala	Ala	Ala	His	Gly	Ala	Gly	Gly	Gly	Pro	Pro	Pro	Ala	Pro	Pro	
		450					455						460				
20	CTC	CCG	GCA	GCA	CAG	GGC	CCT	GGT	GGT	GGG	GGA	GCT	GGG	GCC	CCA	GGC	1440
	Leu	Pro	Ala	Ala	Gln	Gly	Pro	Gly	Gly	Gly	Gly	Ala	Gly	Ala	Pro	Gly	
	465					470					475					480	
25	CTG	GCC	GCA	GCT	ATT	GCT	GGA	GCC	AAA	CTC	AGG	AAA	GTC	AGC	AAG	CAG	1488
	Leu	Ala	Ala	Ala	Ile	Ala	Gly	Ala	Lys	Leu	Arg	Lys	Val	Ser	Lys	Gln	
					485					490					495		
30	GAG	GAG	GCC	TCA	GGG	GGG	CCC	ACA	GCC	CCC	AAA	GCT	GAG	AGT	GGT	CGA	1536
	Glu	Glu	Ala	Ser	Gly	Gly	Pro	Thr	Ala	Pro	Lys	Ala	Glu	Ser	Gly	Arg	
				500					505					510			
35	AGC	GGA	GGT	GGG	GGA	CTC	ATG	GAA	GAG	ATG	AAC	GCC	ATG	CTG	GCC	CGG	1584
	Ser	Gly	Gly	Gly	Gly	Leu	Met	Glu	Glu	Met	Asn	Ala	Met	Leu	Ala	Arg	
			515						520					525			
40	AGA	AGG	AAA	GCC	ACG	CAA	GTT	GGG	GAG	AAA	ACC	CCC	AAG	GAT	GAA	TCT	1632
	Arg	Arg	Lys	Ala	Thr	Gln	Val	Gly	Glu	Lys	Thr	Pro	Lys	Asp	Glu	Ser	
			530				535						540				
45	GCC	AAT	CAG	GAG	GAG	CCA	GAG	GCC	AGA	GTC	CCG	GCC	CAG	AGT	GAA	TCT	1680
	Ala	Asn	Gln	Glu	Glu	Pro	Glu	Ala	Arg	Val	Pro	Ala	Gln	Ser	Glu	Ser	
	545					550					555					560	
50	GTG	CGG	AGA	CCC	TGG	GAG	AAG	AAC	AGC	ACA	ACC	TTG	CCA	AGG	ATG	AAG	1728
	Val	Arg	Arg	Pro	Trp	Glu	Lys	Asn	Ser	Thr	Thr	Leu	Pro	Arg	Met	Lys	
					565					570					575		
55	TCG	TCT	TCT	TCG	GTG	ACC	ACT	TCC	GAG	ACC	CAA	CCC	TGC	ACG	CCC	AGC	1776
	Ser	Ser	Ser	Ser	Val	Thr	Thr	Ser	Glu	Thr	Gln	Pro	Cys	Thr	Pro	Ser	
				580					585					590			
60	TCC	AGT	GAT	TAC	TCG	GAC	CTA	CAG	AGG	GTG	AAA	CAG	GAG	CTT	CTG	GAA	1824
	Ser	Ser	Asp	Tyr	Ser	Asp	Leu	Gln	Arg	Val	Lys	Gln	Glu	Leu	Leu	Glu	
			595					600					605				
65	GAG	GTG	AAG	AAG	GAA	TTG	CAG	AAA	GTG	AAA	GAG	GAA	ATC	ATT	GAA	GCC	1872
	Glu	Val	Lys	Lys	Glu	Leu	Gln	Lys	Val	Lys	Glu	Glu	Ile	Ile	Glu	Ala	
		610					615					620					
70	TTC	GTC	CAG	GAG	CTG	AGG	AAG	CGG	GGT	TCT	CCC	TGA					1908
																	243

244

Phe Val Gln Glu Leu Arg Lys Arg Gly Ser Pro  
625 630 635

5 (2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 635 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10					15		
20	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35					40					45				
25	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
		50					55					60					
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65				70					75					80		
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85						90				95			
30	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
35	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130					135					140					
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145				150					155					160		
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165					170					175			
40	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195				200						205				
45	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215					220					
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230				235					240		
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Met	Ser	Glu	Thr	Val	Ile	Met	
				245					250					255			
50	Ser	Glu	Thr	Val	Ile	Cys	Ser	Ser	Arg	Ala	Thr	Val	Met	Leu	Tyr	Asp	
				260					265					270			
	Asp	Gly	Asn	Lys	Arg	Trp	Leu	Pro	Ala	Gly	Thr	Gly	Pro	Gln	Ala	Phe	
			275				280						285				
55	Ser	Arg	Val	Gln	Ile	Tyr	His	Asn	Pro	Thr	Ala	Asn	Ser	Phe	Arg	Val	
		290				295						300					
	Val	Gly	Arg	Lys	Met	Gln	Pro	Asp	Gln	Gln	Val	Val	Ile	Asn	Cys	Ala	

244



245

305 310 315 320  
 Ile Val Arg Gly Val Lys Tyr Asn Gln Ala Thr Pro Asn Phe His Gln  
 325 330 335  
 5 Trp Arg Asp Ala Arg Gln Val Trp Gly Leu Asn Phe Gly Ser Lys Glu  
 340 345 350  
 Asp Ala Ala Gln Phe Ala Ala Gly Met Ala Ser Ala Leu Glu Ala Leu  
 355 360 365  
 Glu Gly Gly Gly Pro Pro Pro Pro Ala Leu Pro Thr Trp Ser Val  
 370 375 380  
 10 Pro Asn Gly Pro Ser Pro Glu Glu Val Glu Gln Gln Lys Arg Gln Gln  
 385 390 395 400  
 Pro Gly Pro Ser Glu His Ile Glu Arg Arg Val Ser Asn Ala Gly Gly  
 405 410 415  
 15 Pro Pro Ala Pro Pro Ala Gly Gly Pro Pro Pro Pro Pro Gly Pro Pro  
 420 425 430  
 Pro Pro Pro Gly Pro Pro Pro Pro Gly Leu Pro Pro Ser Gly Val  
 435 440 445  
 Pro Ala Ala Ala His Gly Ala Gly Gly Gly Pro Pro Pro Ala Pro Pro  
 450 455 460  
 20 Leu Pro Ala Ala Gln Gly Pro Gly Gly Gly Gly Ala Gly Ala Pro Gly  
 465 470 475 480  
 Leu Ala Ala Ala Ile Ala Gly Ala Lys Leu Arg Lys Val Ser Lys Gln  
 485 490 495  
 25 Glu Glu Ala Ser Gly Gly Pro Thr Ala Pro Lys Ala Glu Ser Gly Arg  
 500 505 510  
 Ser Gly Gly Gly Gly Leu Met Glu Glu Met Asn Ala Met Leu Ala Arg  
 515 520 525  
 Arg Arg Lys Ala Thr Gln Val Gly Glu Lys Thr Pro Lys Asp Glu Ser  
 530 535 540  
 30 Ala Asn Gln Glu Glu Pro Glu Ala Arg Val Pro Ala Gln Ser Glu Ser  
 545 550 555 560  
 Val Arg Arg Pro Trp Glu Lys Asn Ser Thr Thr Leu Pro Arg Met Lys  
 565 570 575  
 35 Ser Ser Ser Ser Val Thr Thr Ser Glu Thr Gln Pro Cys Thr Pro Ser  
 580 585 590  
 Ser Ser Asp Tyr Ser Asp Leu Gln Arg Val Lys Gln Glu Leu Leu Glu  
 595 600 605  
 Glu Val Lys Lys Glu Leu Gln Lys Val Lys Glu Glu Ile Ile Glu Ala  
 610 615 620  
 40 Phe Val Gln Glu Leu Arg Lys Arg Gly Ser Pro  
 625 630 635

## (2) INFORMATION FOR SEQ ID NO:126:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 50  
 (ii) MOLECULE TYPE: cDNA  
 (ix) FEATURE:  
 55 (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...1326  
 (D) OTHER INFORMATION:

245

246

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

5	ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
	Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
	1 5 10 15	
10	GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
	Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
	20 25 30	
15	GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
	Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
	35 40 45	
20	TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
	Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
	50 55 60	
25	CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
	Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
	65 70 75 80	
30	CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
	Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
	85 90 95	
35	CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336
	Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
	100 105 110	
40	GTG AAG TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC	384
	Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
	115 120 125	
45	ATC GAC TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC	432
	Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
	130 135 140	
50	AAC TAC AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC	480
	Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
	145 150 155 160	
55	GGC ATC AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC	528
	Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
	165 170 175	
60	GTG CAG CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC	576
	Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
	180 185 190	
65	CCC GTG CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG	624
	Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
	195 200 205	
70	AGC AAA GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC	672

246

247

	Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
	210 215 220	
5	GTG ACC GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TCC Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	720
	225 230 235 240	
10	GGA CTC AGA TCT CGA GCT CAA GCT TCA ATG GCT GCC ATC CGG AAG AAA Gly Leu Arg Ser Arg Ala Gln Ala Ser Met Ala Ala Ile Arg Lys Lys	768
	245 250 255	
15	CTG GTG ATT GTT GGT GAT GGA GCC TGT GGA AAG ACA TGC TTG CTC ATA Leu Val Ile Val Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile	816
	260 265 270	
20	GTC TTC AGC AAG GAC CAG TTC CCA GAG GTG TAT GTG CCC ACA GTG TTT Val Phe Ser Lys Asp Gln Phe Pro Glu Val Tyr Val Pro Thr Val Phe	864
	275 280 285	
25	GAG AAC TAT GTG GCA GAT ATC GAG GTG GAT GGA AAG CAG GTA GAG TTG Glu Asn Tyr Val Ala Asp Ile Glu Val Asp Gly Lys Gln Val Glu Leu	912
	290 295 300	
30	GCT TTG TGG GAC ACA GCT GGG CAG GAA GAT TAT GAT CGC CTG AGG CCC Ala Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro	960
	305 310 315 320	
35	CTC TCC TAC CCA GAT ACC GAT GTT ATA CTG ATG TGT TTT TCC ATC GAC Leu Ser Tyr Pro Asp Thr Asp Val Ile Leu Met Cys Phe Ser Ile Asp	1008
	325 330 335	
40	AGC CCT GAT AGT TTA GAA AAC ATC CCA GAA AAG TGG ACC CCA GAA GTC Ser Pro Asp Ser Leu Glu Asn Ile Pro Glu Lys Trp Thr Pro Glu Val	1056
	340 345 350	
45	AAG CAT TTC TGT CCC AAC GTG CCC ATC ATC CTG GTT GGG AAT AAG AAG Lys His Phe Cys Pro Asn Val Pro Ile Ile Leu Val Gly Asn Lys Lys	1104
	355 360 365	
50	GAT CTT CGG AAT GAT GAG CAC ACA AGG CGG GAG CTA GCC AAG ATG AAG Asp Leu Arg Asn Asp Glu His Thr Arg Arg Glu Leu Ala Lys Met Lys	1152
	370 375 380	
55	CAG GAG CCG GTG AAA CCT GAA GAA GGC AGA GAT ATG GCA AAC AGG ATT Gln Glu Pro Val Lys Pro Glu Glu Gly Arg Asp Met Ala Asn Arg Ile	1200
	385 390 395 400	
60	GGC GCT TTT GGG TAC ATG GAG TGT TCA GCA AAG ACC AAA GAT GGA GTG Gly Ala Phe Gly Tyr Met Glu Cys Ser Ala Lys Thr Lys Asp Gly Val	1248
	405 410 415	
65	AGA GAG GTT TTT GAA ATG GCT ACG AGA GCT GCT CTG CAA GCT AGA CGT Arg Glu Val Phe Glu Met Ala Thr Arg Ala Ala Leu Gln Ala Arg Arg	1296
	420 425 430	
70	GGG AAG AAA AAA TCT GGT TGC CTT GTC TTG TGA	1329

247

248

Gly Lys Lys Lys Ser Gly Cys Leu Val Leu  
 435 440

5 (2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 442 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10					15		
20	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
				35					40					45			
25	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
		50				55						60					
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70					75					80	
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85					90					95		
30	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
				115				120					125				
35	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130				135						140					
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155					160	
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165					170					175		
40	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180						185				190			
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
				195				200					205				
45	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210				215						220					
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230					235					240	
	Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Met	Ala	Ala	Ile	Arg	Lys	Lys	
					245					250					255		
50	Leu	Val	Ile	Val	Gly	Asp	Gly	Ala	Cys	Gly	Lys	Thr	Cys	Leu	Leu	Ile	
				260				265						270			
	Val	Phe	Ser	Lys	Asp	Gln	Phe	Pro	Glu	Val	Tyr	Val	Pro	Thr	Val	Phe	
				275				280					285				
	Glu	Asn	Tyr	Val	Ala	Asp	Ile	Glu	Val	Asp	Gly	Lys	Gln	Val	Glu	Leu	
55		290				295						300					
	Ala	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	

248

249

	305				310				315					320		
	Leu	Ser	Tyr	Pro	Asp	Thr	Asp	Val	Ile	Leu	Met	Cys	Phe	Ser	Ile	Asp
					325					330					335	
5	Ser	Pro	Asp	Ser	Leu	Glu	Asn	Ile	Pro	Glu	Lys	Trp	Thr	Pro	Glu	Val
				340					345					350		
	Lys	His	Phe	Cys	Pro	Asn	Val	Pro	Ile	Ile	Leu	Val	Gly	Asn	Lys	Lys
			355					360					365			
	Asp	Leu	Arg	Asn	Asp	Glu	His	Thr	Arg	Arg	Glu	Leu	Ala	Lys	Met	Lys
		370						375					380			
10	Gln	Glu	Pro	Val	Lys	Pro	Glu	Glu	Gly	Arg	Asp	Met	Ala	Asn	Arg	Ile
						390					395					400
	Gly	Ala	Phe	Gly	Tyr	Met	Glu	Cys	Ser	Ala	Lys	Thr	Lys	Asp	Gly	Val
				405						410					415	
	Arg	Glu	Val	Phe	Glu	Met	Ala	Thr	Arg	Ala	Ala	Leu	Gln	Ala	Arg	Arg
15				420					425					430		
	Gly	Lys	Lys	Lys	Ser	Gly	Cys	Leu	Val	Leu						
			435					440								

(2) INFORMATION FOR SEQ ID NO:128:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1140 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

30

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1137

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

35

ATG GAC CAT TAT GAT TCT CAG CAA ACC AAC GAT TAC ATG CAG CCA GAA 48  
Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu  
1 5 10 15

40

GAG GAC TGG GAC CGG GAC CTG CTC CTG GAC CCG GCC TGG GAG AAG CAG 96  
Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln  
20 25 30

45

CAG AGA AAG ACA TTC ACG GCA TGG TGT AAC TCC CAC CTC CGG AAG GCG 144  
Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala  
35 40 45

50

GGG ACA CAG ATC GAG AAC ATC GAA GAG GAC TTC CGG GAT GGC CTG AAG 192  
Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys  
50 55 60

55

CTC ATG CTG CTG CTG GAG GTC ATC TCA GGT GAA CGC TTG GCC AAG CCA 240  
Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro  
65 70 75 80

GAG CGA GGC AAG ATG AGA GTG CAC AAG ATC TCC AAC GTC AAC AAG GCC 288

250

	Glu	Arg	Gly	Lys	Met	Arg	Val	His	Lys	Ile	Ser	Asn	Val	Asn	Lys	Ala	
					85					90					95		
5	CTG	GAT	TTC	ATA	GCC	AGC	AAA	GGC	GTC	AAA	CTG	GTG	TCC	ATC	GGA	GCC	336
	Leu	Asp	Phe	Ile	Ala	Ser	Lys	Gly	Val	Lys	Leu	Val	Ser	Ile	Gly	Ala	
				100					105					110			
10	GAA	GAA	ATC	GTG	GAT	GGG	AAT	GTG	AAG	ATG	ACC	CTG	GGC	ATG	ATC	TGG	384
	Glu	Glu	Ile	Val	Asp	Gly	Asn	Val	Lys	Met	Thr	Leu	Gly	Met	Ile	Trp	
			115					120					125				
15	ACC	ATC	ATC	CTG	CGC	AGG	GAT	CCA	CCG	GTC	GCC	ACC	ATG	GTG	AGC	AAG	432
	Thr	Ile	Ile	Leu	Arg	Arg	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	
			130				135					140					
20	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	GTC	GAG	CTG	GAC	480
	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	
	145					150				155						160	
25	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	GAG	GGC	GAG	GGC	528
	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	
				165					170					175			
30	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	TGC	ACC	ACC	GGC	576
	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	
			180					185					190				
35	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	CTG	ACC	TAC	GGC	624
	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	
		195					200						205				
40	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	CAG	CAC	GAC	TTC	672
	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	
		210					215					220					
45	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC	TTC	720
	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	
	225					230				235					240		
50	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	GTG	AAG	TTC	GAG	768
	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	
				245					250						255		
55	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	816
	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	
			260						265					270			
60	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC	TAC	AAC	AGC	864
	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	
			275					280					285				
65	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC	ATC	AAG	GTG	912
	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	
		290					295					300					
70	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	GTG	CAG	CTC	GCC	960

250

251

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 305 310 315 320

5 GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC GTG CTG CTG 1008  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 325 330 335

10 CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA GAC CCC 1056  
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
 340 345 350

AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG ACC GCC GCC 1104  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 355 360 365

15 GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA 1140  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 370 375

20 (2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 379 amino acids  
 25 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
 30 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

35 Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu  
 1 5 10 15  
 Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln  
 20 25 30  
 Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala  
 35 40 45  
 40 Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys  
 50 55 60  
 Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro  
 65 70 75 80  
 Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala  
 45 85 90 95  
 Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala  
 100 105 110  
 Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp  
 115 120 125  
 50 Thr Ile Ile Leu Arg Arg Asp Pro Pro Val Ala Thr Met Val Ser Lys  
 130 135 140  
 Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp  
 145 150 155 160  
 Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly  
 55 165 170 175  
 Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly

251

252

		180		185		190	
	Lys	Leu	Pro	Val	Pro	Trp	Pro
		195		200		205	
5	Val	Gln	Cys	Phe	Ser	Arg	Tyr
		210		215		220	
	Phe	Lys	Ser	Ala	Met	Pro	Glu
	225			230		235	
	Phe	Lys	Asp	Asp	Gly	Asn	Tyr
			245		250		255
10	Gly	Asp	Thr	Leu	Val	Asn	Arg
		260		265		270	
	Glu	Asp	Gly	Asn	Ile	Leu	Gly
		275		280		285	
	His	Asn	Val	Tyr	Ile	Met	Ala
15		290		295		300	
	Asn	Phe	Lys	Ile	Arg	His	Asn
	305			310		315	
	Asp	His	Tyr	Gln	Gln	Asn	Thr
			325		330		335
20	Pro	Asp	Asn	His	Tyr	Leu	Ser
		340		345		350	
	Asn	Glu	Lys	Arg	Asp	His	Met
		355		360		365	
25	Gly	Ile	Thr	Leu	Gly	Met	Asp
		370		375			

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 3516 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...3513  
 40 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC	GGG	GTG	GTG	CCC	ATC	CTG	48
45	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1			5				10						15			
	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	96
	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
50			20				25					30					
	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	144
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35				40					45						
55	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	192

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253

	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50						55					60					
5	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	240
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65				70					75					80		
10	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	288
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90						95		
15	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
				115				120					125				
20	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
				130			135					140					
25	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155					160	
30	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165				170						175		
35	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180				185						190			
	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
				195				200					205				
40	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
				210			215					220					
45	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230					235					240	
50	GGA	CTC	AGA	TCT	CGA	GCC	ATG	AAC	GCC	CCC	GAG	CGG	CAG	CCC	CAA	CCC	768
	Gly	Leu	Arg	Ser	Arg	Ala	Met	Asn	Ala	Pro	Glu	Arg	Gln	Pro	Gln	Pro	
					245					250					255		
55	GAC	GGC	GGG	GAC	GCC	CCA	GGC	CAC	GAG	CCT	GGG	GGC	AGC	CCC	CAA	GAC	816
	Asp	Gly	Gly	Asp	Ala	Pro	Gly	His	Glu	Pro	Gly	Gly	Ser	Pro	Gln	Asp	
				260					265					270			
	GAG	CTT	GAC	TTC	TCC	ATC	CTC	TTC	GAC	TAT	GAG	TAT	TTG	AAT	CCG	AAC	864

253

254

	Glu	Leu	Asp	Phe	Ser	Ile	Leu	Phe	Asp	Tyr	Glu	Tyr	Leu	Asn	Pro	Asn	
			275					280					285				
5	GAA	GAA	GAG	CCG	AAT	GCA	CAT	AAG	GTC	GCC	AGC	CCA	CCC	TCC	GGA	CCC	912
	Glu	Glu	Glu	Pro	Asn	Ala	His	Lys	Val	Ala	Ser	Pro	Pro	Ser	Gly	Pro	
			290				295				300						
10	GCA	TAC	CCC	GAT	GAT	GTA	ATG	GAC	TAT	GGC	CTC	AAG	CCA	TAC	AGC	CCC	960
	Ala	Tyr	Pro	Asp	Asp	Val	Met	Asp	Tyr	Gly	Leu	Lys	Pro	Tyr	Ser	Pro	
	305					310					315					320	
15	CTT	GCT	AGT	CTC	TCT	GGC	GAG	CCC	CCC	GGC	CGA	TTC	GGA	GAG	CCG	GAT	1008
	Leu	Ala	Ser	Leu	Ser	Gly	Glu	Pro	Pro	Gly	Arg	Phe	Gly	Glu	Pro	Asp	
					325					330					335		
20	AGG	GTA	GGG	CCG	CAG	AAG	TTT	CTG	AGC	GCG	GCC	AAG	CCA	GCA	GGG	GCC	1056
	Arg	Val	Gly	Pro	Gln	Lys	Phe	Leu	Ser	Ala	Ala	Lys	Pro	Ala	Gly	Ala	
				340					345				350				
25	TCG	GGC	CTG	AGC	CCT	CGG	ATC	GAG	ATC	ACT	CCG	TCC	CAC	GAA	CTG	ATC	1104
	Ser	Gly	Leu	Ser	Pro	Arg	Ile	Glu	Ile	Thr	Pro	Ser	His	Glu	Leu	Ile	
			355				360						365				
30	CAG	GCA	GTG	GGG	CCC	CTC	CGC	ATG	AGA	GAC	GCG	GGC	CTC	CTG	GTG	GAG	1152
	Gln	Ala	Val	Gly	Pro	Leu	Arg	Met	Arg	Asp	Ala	Gly	Leu	Leu	Val	Glu	
			370				375					380					
35	CAG	CCT	CCC	CTG	GCC	GGG	GTG	GCC	GCC	AGC	CCG	AGG	TTC	ACC	CTG	CCC	1200
	Gln	Pro	Pro	Leu	Ala	Gly	Val	Ala	Ala	Ser	Pro	Arg	Phe	Thr	Leu	Pro	
	385					390					395					400	
40	GTG	CCC	GGC	TTC	GAG	GGC	TAC	CGC	GAG	CCG	CTT	TGC	TTG	AGC	CCC	GCT	1248
	Val	Pro	Gly	Phe	Glu	Gly	Tyr	Arg	Glu	Pro	Leu	Cys	Leu	Ser	Pro	Ala	
					405					410					415		
45	AGC	AGC	GGC	TCC	TCT	GCC	AGC	TTC	ATT	TCT	GAC	ACC	TTC	TCC	CCC	TAC	1296
	Ser	Ser	Gly	Ser	Ser	Ala	Ser	Phe	Ile	Ser	Asp	Thr	Phe	Ser	Pro	Tyr	
				420				425					430				
50	ACC	TCG	CCC	TGC	GTC	TCG	CCC	AAT	AAC	GGC	GGG	CCC	GAC	GAC	CTG	TGT	1344
	Thr	Ser	Pro	Cys	Val	Ser	Pro	Asn	Asn	Gly	Gly	Pro	Asp	Asp	Leu	Cys	
			435				440						445				
55	CCG	CAG	TTT	CAA	AAC	ATC	CCT	GCT	CAT	TAT	TCC	CCC	AGA	ACC	TCG	CCA	1392
	Pro	Gln	Phe	Gln	Asn	Ile	Pro	Ala	His	Tyr	Ser	Pro	Arg	Thr	Ser	Pro	
			450				455					460					
60	ATA	ATG	TCA	CCT	CGA	ACC	AGC	CTC	GCC	GAG	GAC	AGC	TGC	CTG	GGC	CGC	1440
	Ile	Met	Ser	Pro	Arg	Thr	Ser	Leu	Ala	Glu	Asp	Ser	Cys	Leu	Gly	Arg	
	465					470					475					480	
65	CAC	TCG	CCC	GTG	CCC	CGT	CCG	GCC	TCC	CGC	TCC	TCA	TCG	CCT	GGT	GCC	1488
	His	Ser	Pro	Val	Pro	Arg	Pro	Ala	Ser	Arg	Ser	Ser	Ser	Pro	Gly	Ala	
					485					490					495		
70	AAG	CGG	AGG	CAT	TCG	TGC	GCC	GAG	GCC	TTG	GTT	GCC	CTG	CCG	CCC	GGA	1536

254

255

	Lys	Arg	Arg	His	Ser	Cys	Ala	Glu	Ala	Leu	Val	Ala	Leu	Pro	Pro	Gly	
				500					505					510			
5	GCC	TCA	CCC	CAG	CGC	TCC	CGG	AGC	CCC	TCG	CCG	CAG	CCC	TCA	TCT	CAC	1584
	Ala	Ser	Pro	Gln	Arg	Ser	Arg	Ser	Pro	Ser	Pro	Gln	Pro	Ser	Ser	His	
			515					520					525				
10	GTG	GCA	CCC	CAG	GAC	CAC	GGC	TCC	CCG	GCT	GGG	TAC	CCC	CCT	GTG	GCT	1632
	Val	Ala	Pro	Gln	Asp	His	Gly	Ser	Pro	Ala	Gly	Tyr	Pro	Pro	Val	Ala	
		530					535					540					
15	GGC	TCT	GCC	GTG	ATC	ATG	GAT	GCC	CTG	AAC	AGC	CTC	GCC	ACG	GAC	TCG	1680
	Gly	Ser	Ala	Val	Ile	Met	Asp	Ala	Leu	Asn	Ser	Leu	Ala	Thr	Asp	Ser	
	545					550					555				560		
	CCT	TGT	GGG	ATC	CCC	CCC	AAG	ATG	TGG	AAG	ACC	AGC	CCT	GAC	CCC	TCG	1728
	Pro	Cys	Gly	Ile	Pro	Pro	Lys	Met	Trp	Lys	Thr	Ser	Pro	Asp	Pro	Ser	
				565					570					575			
20	CCG	GTG	TCT	GCC	GCC	CCA	TCC	AAG	GCC	GGC	CTG	CCT	CGC	CAC	ATC	TAC	1776
	Pro	Val	Ser	Ala	Ala	Pro	Ser	Lys	Ala	Gly	Leu	Pro	Arg	His	Ile	Tyr	
				580					585					590			
25	CCG	GCC	GTG	GAG	TTC	CTG	GGG	CCC	TGC	GAG	CAG	GGC	GAG	AGG	AGA	AAC	1824
	Pro	Ala	Val	Glu	Phe	Leu	Gly	Pro	Cys	Glu	Gln	Gly	Glu	Arg	Arg	Asn	
			595				600						605				
30	TCG	GCT	CCA	GAA	TCC	ATC	CTG	CTG	GTT	CCG	CCC	ACT	TGG	CCC	AAG	CCG	1872
	Ser	Ala	Pro	Glu	Ser	Ile	Leu	Leu	Val	Pro	Pro	Thr	Trp	Pro	Lys	Pro	
		610					615					620					
35	CTG	GTG	CCT	GCC	ATT	CCC	ATC	TGC	AGC	ATC	CCA	GTG	ACT	GCA	TCC	CTC	1920
	Leu	Val	Pro	Ala	Ile	Pro	Ile	Cys	Ser	Ile	Pro	Val	Thr	Ala	Ser	Leu	
	625					630					635				640		
	CCT	CCA	CTT	GAG	TGG	CCG	CTG	TCC	AGT	CAG	TCA	GGC	TCT	TAC	GAG	CTG	1968
	Pro	Pro	Leu	Glu	Trp	Pro	Leu	Ser	Ser	Gln	Ser	Gly	Ser	Tyr	Glu	Leu	
				645					650					655			
40	CGG	ATC	GAG	GTG	CAG	CCC	AAG	CCA	CAT	CAC	CGG	GCC	CAC	TAT	GAG	ACA	2016
	Arg	Ile	Glu	Val	Gln	Pro	Lys	Pro	His	His	Arg	Ala	His	Tyr	Glu	Thr	
				660					665					670			
45	GAA	GGC	AGC	CGA	GGG	GCT	GTC	AAA	GCT	CCA	ACT	GGA	GGC	CAC	CCT	GTG	2064
	Glu	Gly	Ser	Arg	Gly	Ala	Val	Lys	Ala	Pro	Thr	Gly	Gly	His	Pro	Val	
			675					680					685				
50	GTT	CAG	CTC	CAT	GGC	TAC	ATG	GAA	AAC	AAG	CCT	CTG	GGA	CTT	CAG	ATC	2112
	Val	Gln	Leu	His	Gly	Tyr	Met	Glu	Asn	Lys	Pro	Leu	Gly	Leu	Gln	Ile	
		690					695				700						
55	TTC	ATT	GGG	ACA	GCT	GAT	GAG	CGG	ATC	CTT	AAG	CCG	CAC	GCC	TTC	TAC	2160
	Phe	Ile	Gly	Thr	Ala	Asp	Glu	Arg	Ile	Leu	Lys	Pro	His	Ala	Phe	Tyr	
	705				710						715				720		
	CAG	GTG	CAC	CGA	ATC	ACG	GGG	AAA	ACT	GTC	ACC	ACC	ACC	AGC	TAT	GAG	2208

255

256

	Gln	Val	His	Arg	Ile	Thr	Gly	Lys	Thr	Val	Thr	Thr	Thr	Ser	Tyr	Glu	
					725					730						735	
5	AAG	ATA	GTG	GGC	AAC	ACC	AAA	GTC	CTG	GAG	ATC	CCC	TTG	GAG	CCC	AAA	2256
	Lys	Ile	Val	Gly	Asn	Thr	Lys	Val	Leu	Glu	Ile	Pro	Leu	Glu	Pro	Lys	
				740					745					750			
10	AAC	AAC	ATG	AGG	GCA	ACC	ATC	GAC	TGT	GCG	GGG	ATC	TTG	AAG	CTT	AGA	2304
	Asn	Asn	Met	Arg	Ala	Thr	Ile	Asp	Cys	Ala	Gly	Ile	Leu	Lys	Leu	Arg	
			755					760					765				
15	AAC	GCC	GAC	ATT	GAG	CTG	CGG	AAA	GGC	GAG	ACG	GAC	ATT	GGA	AGA	AAG	2352
	Asn	Ala	Asp	Ile	Glu	Leu	Arg	Lys	Gly	Glu	Thr	Asp	Ile	Gly	Arg	Lys	
		770					775					780					
20	AAC	ACG	CGG	GTG	AGA	CTG	GTT	TTC	CGA	GTT	CAC	ATC	CCA	GAG	TCC	AGT	2400
	Asn	Thr	Arg	Val	Arg	Leu	Val	Phe	Arg	Val	His	Ile	Pro	Glu	Ser	Ser	
		785				790				795						800	
25	GGC	AGA	ATC	GTC	TCT	TTA	CAG	ACT	GCA	TCT	AAC	CCC	ATC	GAG	TGC	TCC	2448
	Gly	Arg	Ile	Val	Ser	Leu	Gln	Thr	Ala	Ser	Asn	Pro	Ile	Glu	Cys	Ser	
				805						810					815		
30	CAG	CGA	TCT	GCT	CAC	GAG	CTG	CCC	ATG	GTT	GAA	AGA	CAA	GAC	ACA	GAC	2496
	Gln	Arg	Ser	Ala	His	Glu	Leu	Pro	Met	Val	Glu	Arg	Gln	Asp	Thr	Asp	
			820					825						830			
35	AGC	TGC	CTG	GTC	TAT	GGC	GGC	CAG	CAA	ATG	ATC	CTC	ACG	GGG	CAG	AAC	2544
	Ser	Cys	Leu	Val	Tyr	Gly	Gly	Gln	Gln	Met	Ile	Leu	Thr	Gly	Gln	Asn	
			835					840					845				
40	TTT	ACA	TCC	GAG	TCC	AAA	GTT	GTG	TTT	ACT	GAG	AAG	ACC	ACA	GAT	GGA	2592
	Phe	Thr	Ser	Glu	Ser	Lys	Val	Phe	Thr	Glu	Lys	Thr	Thr	Asp	Gly		
		850					855					860					
45	CAG	CAA	ATT	TGG	GAG	ATG	GAA	GCC	ACG	GTG	GAT	AAG	GAC	AAG	AGC	CAG	2640
	Gln	Gln	Ile	Trp	Glu	Met	Glu	Ala	Thr	Val	Asp	Lys	Asp	Lys	Ser	Gln	
		865				870				875					880		
50	CCC	AAC	ATG	CTT	TTT	GTT	GAG	ATC	CCT	GAA	TAT	CGG	AAC	AAG	CAT	ATC	2688
	Pro	Asn	Met	Leu	Phe	Val	Glu	Ile	Pro	Glu	Tyr	Arg	Asn	Lys	His	Ile	
				885				890						895			
55	CGC	ACA	CCT	GTA	AAA	GTG	AAC	TTC	TAC	GTC	ATC	AAT	GGG	AAG	AGA	AAA	2736
	Arg	Thr	Pro	Val	Lys	Val	Asn	Phe	Tyr	Val	Ile	Asn	Gly	Lys	Arg	Lys	
			900					905						910			
60	CGA	AGT	CAG	CCT	CAG	CAC	TTT	ACC	TAC	CAC	CCA	GTC	CCA	GCC	ATC	AAG	2784
	Arg	Ser	Gln	Pro	Gln	His	Phe	Thr	Tyr	His	Pro	Val	Pro	Ala	Ile	Lys	
			915					920					925				
65	ACG	GAG	CCC	ACG	GAT	GAA	TAT	GAC	CCC	ACT	CTG	ATC	TGC	AGC	CCC	ACC	2832
	Thr	Glu	Pro	Thr	Asp	Glu	Tyr	Asp	Pro	Thr	Leu	Ile	Cys	Ser	Pro	Thr	
		930					935					940					
70	CAT	GGA	GGC	CTG	GGG	AGC	CAG	CCT	TAC	TAC	CCC	CAG	CAC	CCG	ATG	GTG	2880

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	His Gly Gly Leu Gly Ser Gln Pro Tyr Tyr Pro Gln His Pro Met Val	
	945 950 955 960	
5	GCC GAG TCC CCC TCC TGC CTC GTG GCC ACC ATG GCT CCC TGC CAG CAG Ala Glu Ser Pro Ser Cys Leu Val Ala Thr Met Ala Pro Cys Gln Gln	2928
	965 970 975	
10	TTC CGC ACG GGG CTC TCA TCC CCT GAC GCC CGC TAC CAG CAA CAG AAC Phe Arg Thr Gly Leu Ser Ser Pro Asp Ala Arg Tyr Gln Gln Gln Asn	2976
	980 985 990	
15	CCA GCG GCC GTA CTC TAC CAG CGG AGC AAG AGC CTG AGC CCC AGC CTG Pro Ala Ala Val Leu Tyr Gln Arg Ser Lys Ser Leu Ser Pro Ser Leu	3024
	995 1000 1005	
	CTG GGC TAT CAG CAG CCG GCC CTC ATG GCC GCC CCG CTG TCC CTT GCG Leu Gly Tyr Gln Gln Pro Ala Leu Met Ala Ala Pro Leu Ser Leu Ala	3072
	1010 1015 1020	
20	GAC GCT CAC CGC TCT GTG CTG GTG CAC GCC GGC TCC CAG GGC CAG AGC Asp Ala His Arg Ser Val Leu Val His Ala Gly Ser Gln Gly Gln Ser	3120
	1025 1030 1035 1040	
25	TCA GCC CTG CTC CAC CCC TCT CCG ACC AAC CAG CAG GCC TCG CCT GTG Ser Ala Leu Leu His Pro Ser Pro Thr Asn Gln Gln Ala Ser Pro Val	3168
	1045 1050 1055	
30	ATC CAC TAC TCA CCC ACC AAC CAG CAG CTG CGC TGC GGA AGC CAC CAG Ile His Tyr Ser Pro Thr Asn Gln Gln Leu Arg Cys Gly Ser His Gln	3216
	1060 1065 1070	
35	GAG TTC CAG CAC ATC ATG TAC TGC GAG AAT TTC GCA CCA GGC ACC ACC Glu Phe Gln His Ile Met Tyr Cys Glu Asn Phe Ala Pro Gly Thr Thr	3264
	1075 1080 1085	
	AGA CCT GGC CCG CCC CCG GTC AGT CAA GGT CAG AGG CTG AGC CCG GGT Arg Pro Gly Pro Pro Pro Val Ser Gln Gly Gln Arg Leu Ser Pro Gly	3312
	1090 1095 1100	
40	TCC TAC CCC ACA GTC ATT CAG CAG CAG AAT GCC ACG AGC CAA AGA GCC Ser Tyr Pro Thr Val Ile Gln Gln Gln Asn Ala Thr Ser Gln Arg Ala	3360
	1105 1110 1115 1120	
45	GCC AAA AAC GGA CCC CCG GTC AGT GAC CAA AAG GAA GTA TTA CCT GCG Ala Lys Asn Gly Pro Pro Val Ser Asp Gln Lys Glu Val Leu Pro Ala	3408
	1125 1130 1135	
50	GGG GTG ACC ATT AAA CAG GAG CAG AAC TTG GAC CAG ACC TAC TTG GAT Gly Val Thr Ile Lys Gln Glu Gln Asn Leu Asp Gln Thr Tyr Leu Asp	3456
	1140 1145 1150	
	GAT GTT AAT GAA ATT ATC AGG AAG GAG TTT TCA GGA CCT CCT GCC AGA Asp Val Asn Glu Ile Ile Arg Lys Glu Phe Ser Gly Pro Pro Ala Arg	3504
	1155 1160 1165	
55	AAT CAG ACG TAA	3516

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Asn Gln Thr  
1170

5 (2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1171 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10					15		
20	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
				35					40					45			
	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
25		50					55				60						
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70					75					80	
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85					90					95		
30	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
				115					120					125			
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
35		130					135					140					
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150					155					160	
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165					170					175		
40	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180						185				190			
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
				195					200					205			
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
45		210					215					220					
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230					235					240	
	Gly	Leu	Arg	Ser	Arg	Ala	Met	Asn	Ala	Pro	Glu	Arg	Gln	Pro	Gln	Pro	
					245					250					255		
50	Asp	Gly	Gly	Asp	Ala	Pro	Gly	His	Glu	Pro	Gly	Gly	Ser	Pro	Gln	Asp	
				260					265					270			
	Glu	Leu	Asp	Phe	Ser	Ile	Leu	Phe	Asp	Tyr	Glu	Tyr	Leu	Asn	Pro	Asn	
				275				280					285				
	Glu	Glu	Glu	Pro	Asn	Ala	His	Lys	Val	Ala	Ser	Pro	Pro	Ser	Gly	Pro	
55		290					295					300					
	Ala	Tyr	Pro	Asp	Asp	Val	Met	Asp	Tyr	Gly	Leu	Lys	Pro	Tyr	Ser	Pro	

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	305				310				315				320
	Leu	Ala	Ser	Leu	Ser	Gly	Glu	Pro	Pro	Gly	Arg	Phe	Gly
					325				330				335
5	Arg	Val	Gly	Pro	Gln	Lys	Phe	Leu	Ser	Ala	Ala	Lys	Pro
				340					345				350
	Ser	Gly	Leu	Ser	Pro	Arg	Ile	Glu	Ile	Thr	Pro	Ser	His
			355					360				365	
	Gln	Ala	Val	Gly	Pro	Leu	Arg	Met	Arg	Asp	Ala	Gly	Leu
		370					375				380		
10	Gln	Pro	Pro	Leu	Ala	Gly	Val	Ala	Ala	Ser	Pro	Arg	Phe
		385					390				395		400
	Val	Pro	Gly	Phe	Glu	Gly	Tyr	Arg	Glu	Pro	Leu	Cys	Leu
				405					410				415
	Ser	Ser	Gly	Ser	Ser	Ala	Ser	Phe	Ile	Ser	Asp	Thr	Phe
15				420					425				430
	Thr	Ser	Pro	Cys	Val	Ser	Pro	Asn	Asn	Gly	Gly	Pro	Asp
			435					440				445	
	Pro	Gln	Phe	Gln	Asn	Ile	Pro	Ala	His	Tyr	Ser	Pro	Arg
		450					455				460		
20	Ile	Met	Ser	Pro	Arg	Thr	Ser	Leu	Ala	Glu	Asp	Ser	Cys
		465					470				475		480
	His	Ser	Pro	Val	Pro	Arg	Pro	Ala	Ser	Arg	Ser	Ser	Ser
				485					490				495
	Lys	Arg	Arg	His	Ser	Cys	Ala	Glu	Ala	Leu	Val	Ala	Leu
25				500					505				510
	Ala	Ser	Pro	Gln	Arg	Ser	Arg	Ser	Pro	Ser	Pro	Gln	Pro
			515					520				525	
	Val	Ala	Pro	Gln	Asp	His	Gly	Ser	Pro	Ala	Gly	Tyr	Pro
		530					535				540		
30	Gly	Ser	Ala	Val	Ile	Met	Asp	Ala	Leu	Asn	Ser	Leu	Ala
		545				550				555			560
	Pro	Cys	Gly	Ile	Pro	Pro	Lys	Met	Trp	Lys	Thr	Ser	Pro
				565					570				575
	Pro	Val	Ser	Ala	Ala	Pro	Ser	Lys	Ala	Gly	Leu	Pro	Arg
35				580					585				590
	Pro	Ala	Val	Glu	Phe	Leu	Gly	Pro	Cys	Glu	Gln	Gly	Glu
			595					600				605	
	Ser	Ala	Pro	Glu	Ser	Ile	Leu	Leu	Val	Pro	Pro	Thr	Trp
		610					615					620	
40	Leu	Val	Pro	Ala	Ile	Pro	Ile	Cys	Ser	Ile	Pro	Val	Thr
		625				630					635		640
	Pro	Pro	Leu	Glu	Trp	Pro	Leu	Ser	Ser	Gln	Ser	Gly	Ser
				645					650				655
	Arg	Ile	Glu	Val	Gln	Pro	Lys	Pro	His	His	Arg	Ala	His
45				660					665				670
	Glu	Gly	Ser	Arg	Gly	Ala	Val	Lys	Ala	Pro	Thr	Gly	Gly
			675					680				685	
	Val	Gln	Leu	His	Gly	Tyr	Met	Glu	Asn	Lys	Pro	Leu	Gly
		690					695				700		
50	Phe	Ile	Gly	Thr	Ala	Asp	Glu	Arg	Ile	Leu	Lys	Pro	His
		705				710					715		720
	Gln	Val	His	Arg	Ile	Thr	Gly	Lys	Thr	Val	Thr	Thr	Thr
				725					730				735
	Lys	Ile	Val	Gly	Asn	Thr	Lys	Val	Leu	Glu	Ile	Pro	Leu
55				740					745				750
	Asn	Asn	Met	Arg	Ala	Thr	Ile	Asp	Cys	Ala	Gly	Ile	Leu

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	755		760		765
	Asn Ala Asp Ile Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys				
	770		775		780
5	Asn Thr Arg Val Arg Leu Val Phe Arg Val His Ile Pro Glu Ser Ser				
	785		790		795
	Gly Arg Ile Val Ser Leu Gln Thr Ala Ser Asn Pro Ile Glu Cys Ser				800
		805		810	815
	Gln Arg Ser Ala His Glu Leu Pro Met Val Glu Arg Gln Asp Thr Asp				
		820		825	830
10	Ser Cys Leu Val Tyr Gly Gly Gln Gln Met Ile Leu Thr Gly Gln Asn				
		835		840	845
	Phe Thr Ser Glu Ser Lys Val Val Phe Thr Glu Lys Thr Thr Asp Gly				
		850		855	860
15	Gln Gln Ile Trp Glu Met Glu Ala Thr Val Asp Lys Asp Lys Ser Gln				
		865		870	875
	Pro Asn Met Leu Phe Val Glu Ile Pro Glu Tyr Arg Asn Lys His Ile				880
		885		890	895
	Arg Thr Pro Val Lys Val Asn Phe Tyr Val Ile Asn Gly Lys Arg Lys				
		900		905	910
20	Arg Ser Gln Pro Gln His Phe Thr Tyr His Pro Val Pro Ala Ile Lys				
		915		920	925
	Thr Glu Pro Thr Asp Glu Tyr Asp Pro Thr Leu Ile Cys Ser Pro Thr				
		930		935	940
25	His Gly Gly Leu Gly Ser Gln Pro Tyr Tyr Pro Gln His Pro Met Val				
		945		950	955
	Ala Glu Ser Pro Ser Cys Leu Val Ala Thr Met Ala Pro Cys Gln Gln				960
		965		970	975
	Phe Arg Thr Gly Leu Ser Ser Pro Asp Ala Arg Tyr Gln Gln Gln Asn				
		980		985	990
30	Pro Ala Ala Val Leu Tyr Gln Arg Ser Lys Ser Leu Ser Pro Ser Leu				
		995		1000	1005
	Leu Gly Tyr Gln Gln Pro Ala Leu Met Ala Ala Pro Leu Ser Leu Ala				
		1010		1015	1020
35	Asp Ala His Arg Ser Val Leu Val His Ala Gly Ser Gln Gly Gln Ser				
		025		1030	1035
	Ser Ala Leu Leu His Pro Ser Pro Thr Asn Gln Gln Ala Ser Pro Val				1040
		1045		1050	1055
	Ile His Tyr Ser Pro Thr Asn Gln Gln Leu Arg Cys Gly Ser His Gln				
		1060		1065	1070
40	Glu Phe Gln His Ile Met Tyr Cys Glu Asn Phe Ala Pro Gly Thr Thr				
		1075		1080	1085
	Arg Pro Gly Pro Pro Pro Val Ser Gln Gly Gln Arg Leu Ser Pro Gly				
		1090		1095	1100
45	Ser Tyr Pro Thr Val Ile Gln Gln Gln Asn Ala Thr Ser Gln Arg Ala				
		105		1110	1115
	Ala Lys Asn Gly Pro Pro Val Ser Asp Gln Lys Glu Val Leu Pro Ala				1120
		1125		1130	1135
	Gly Val Thr Ile Lys Gln Glu Gln Asn Leu Asp Gln Thr Tyr Leu Asp				
		1140		1145	1150
50	Asp Val Asn Glu Ile Ile Arg Lys Glu Phe Ser Gly Pro Pro Ala Arg				
		1155		1160	1165
	Asn Gln Thr				
		1170			

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(2) INFORMATION FOR SEQ ID NO:132:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3546 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...3543  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

15	ATG AAC GCC CCC GAG CGG CAG CCC CAA CCC GAC GGC GGG GAC GCC CCA	48
	Met Asn Ala Pro Glu Arg Gln Pro Gln Pro Asp Gly Gly Asp Ala Pro	
	1 5 10 15	
20	GGC CAC GAG CCT GGG GGC AGC CCC CAA GAC GAG CTT GAC TTC TCC ATC	96
	Gly His Glu Pro Gly Gly Ser Pro Gln Asp Glu Leu Asp Phe Ser Ile	
	20 25 30	
25	CTC TTC GAC TAT GAG TAT TTG AAT CCG AAC GAA GAA GAG CCG AAT GCA	144
	Leu Phe Asp Tyr Glu Tyr Leu Asn Pro Asn Glu Glu Glu Pro Asn Ala	
	35 40 45	
30	CAT AAG GTC GCC AGC CCA CCC TCC GGA CCC GCA TAC CCC GAT GAT GTA	192
	His Lys Val Ala Ser Pro Pro Ser Gly Pro Ala Tyr Pro Asp Asp Val	
	50 55 60	
35	ATG GAC TAT GGC CTC AAG CCA TAC AGC CCC CTT GCT AGT CTC TCT GGC	240
	Met Asp Tyr Gly Leu Lys Pro Tyr Ser Pro Leu Ala Ser Leu Ser Gly	
	65 70 75 80	
40	GAG CCC CCC GGC CGA TTC GGA GAG CCG GAT AGG GTA GGG CCG CAG AAG	288
	Glu Pro Pro Gly Arg Phe Gly Glu Pro Asp Arg Val Gly Pro Gln Lys	
	85 90 95	
45	TTT CTG AGC GCG GCC AAG CCA GCA GGG GCC TCG GGC CTG AGC CCT CGG	336
	Phe Leu Ser Ala Ala Lys Pro Ala Gly Ala Ser Gly Leu Ser Pro Arg	
	100 105 110	
50	ATC GAG ATC ACT CCG TCC CAC GAA CTG ATC CAG GCA GTG GGG CCC CTC	384
	Ile Glu Ile Thr Pro Ser His Glu Leu Ile Gln Ala Val Gly Pro Leu	
	115 120 125	
55	CGC ATG AGA GAC GCG GGC CTC CTG GTG GAG CAG CCT CCC CTG GCC GGG	432
	Arg Met Arg Asp Ala Gly Leu Leu Val Glu Gln Pro Pro Leu Ala Gly	
	130 135 140	
55	GTG GCC GCC AGC CCG AGG TTC ACC CTG CCC GTG CCC GGC TTC GAG GGC	480
	Val Ala Ala Ser Pro Arg Phe Thr Leu Pro Val Pro Gly Phe Glu Gly	
	145 150 155 160	
	TAC CGC GAG CCG CTT TGC TTG AGC CCC GCT AGC AGC GGC TCC TCT GCC	528

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	Tyr	Arg	Glu	Pro	Leu	Cys	Leu	Ser	Pro	Ala	Ser	Ser	Gly	Ser	Ser	Ala	
					165					170						175	
5	AGC	TTC	ATT	TCT	GAC	ACC	TTC	TCC	CCC	TAC	ACC	TCG	CCC	TGC	GTC	TCG	576
	Ser	Phe	Ile	Ser	Asp	Thr	Phe	Ser	Pro	Tyr	Thr	Ser	Pro	Cys	Val	Ser	
				180					185					190			
10	CCC	AAT	AAC	GGC	GGG	CCC	GAC	GAC	CTG	TGT	CCG	CAG	TTT	CAA	AAC	ATC	624
	Pro	Asn	Asn	Gly	Gly	Pro	Asp	Asp	Leu	Cys	Pro	Gln	Phe	Gln	Asn	Ile	
		195					200					205					
15	CCT	GCT	CAT	TAT	TCC	CCC	AGA	ACC	TCG	CCA	ATA	ATG	TCA	CCT	CGA	ACC	672
	Pro	Ala	His	Tyr	Ser	Pro	Arg	Thr	Ser	Pro	Ile	Met	Ser	Pro	Arg	Thr	
		210					215					220					
20	AGC	CTC	GCC	GAG	GAC	AGC	TGC	CTG	GGC	CGC	CAC	TCG	CCC	GTG	CCC	CGT	720
	Ser	Leu	Ala	Glu	Asp	Ser	Cys	Leu	Gly	Arg	His	Ser	Pro	Val	Pro	Arg	
	225					230				235						240	
25	CCG	GCC	TCC	CGC	TCC	TCA	TCG	CCT	GGT	GCC	AAG	CGG	AGG	CAT	TCG	TGC	768
	Pro	Ala	Ser	Arg	Ser	Ser	Ser	Pro	Gly	Ala	Lys	Arg	Arg	His	Ser	Cys	
					245					250					255		
30	GCC	GAG	GCC	TTG	GTT	GCC	CTG	CCG	CCC	GGA	GCC	TCA	CCC	CAG	CGC	TCC	816
	Ala	Glu	Ala	Leu	Val	Ala	Leu	Pro	Pro	Gly	Ala	Ser	Pro	Gln	Arg	Ser	
				260					265					270			
35	CGG	AGC	CCC	TCG	CCG	CAG	CCC	TCA	TCT	CAC	GTG	GCA	CCC	CAG	GAC	CAC	864
	Arg	Ser	Pro	Ser	Pro	Gln	Pro	Ser	Ser	His	Val	Ala	Pro	Gln	Asp	His	
			275				280						285				
40	GGC	TCC	CCG	GCT	GGG	TAC	CCC	CCT	GTG	GCT	GGC	TCT	GCC	GTG	ATC	ATG	912
	Gly	Ser	Pro	Ala	Gly	Tyr	Pro	Pro	Val	Ala	Gly	Ser	Ala	Val	Ile	Met	
		290					295					300					
45	GAT	GCC	CTG	AAC	AGC	CTC	GCC	ACG	GAC	TCG	CCT	TGT	GGG	ATC	CCC	CCC	960
	Asp	Ala	Leu	Asn	Ser	Leu	Ala	Thr	Asp	Ser	Pro	Cys	Gly	Ile	Pro	Pro	
	305					310				315					320		
50	AAG	ATG	TGG	AAG	ACC	AGC	CCT	GAC	CCC	TCG	CCG	GTG	TCT	GCC	GCC	CCA	1008
	Lys	Met	Trp	Lys	Thr	Ser	Pro	Asp	Pro	Ser	Pro	Val	Ser	Ala	Ala	Pro	
					325				330					335			
55	TCC	AAG	GCC	GGC	CTG	CCT	CGC	CAC	ATC	TAC	CCG	GCC	GTG	GAG	TTC	CTG	1056
	Ser	Lys	Ala	Gly	Leu	Pro	Arg	His	Ile	Tyr	Pro	Ala	Val	Glu	Phe	Leu	
				340					345					350			
60	GGG	CCC	TGC	GAG	CAG	GGC	GAG	AGG	AGA	AAC	TCG	GCT	CCA	GAA	TCC	ATC	1104
	Gly	Pro	Cys	Glu	Gln	Gly	Glu	Arg	Arg	Asn	Ser	Ala	Pro	Glu	Ser	Ile	
		355					360					365					
65	CTG	CTG	GTT	CCG	CCC	ACT	TGG	CCC	AAG	CCG	CTG	GTG	CCT	GCC	ATT	CCC	1152
	Leu	Leu	Val	Pro	Pro	Thr	Trp	Pro	Lys	Pro	Leu	Val	Pro	Ala	Ile	Pro	
		370					375					380					
70	ATC	TGC	AGC	ATC	CCA	GTG	ACT	GCA	TCC	CTC	CCT	CCA	CTT	GAG	TGG	CCG	1200

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	Ile Cys Ser Ile Pro Val Thr Ala Ser Leu Pro Pro Leu Glu Trp Pro	
	385 390 395 400	
5	CTG TCC AGT CAG TCA GGC TCT TAC GAG CTG CGG ATC GAG GTG CAG CCC Leu Ser Ser Gln Ser Gly Ser Tyr Glu Leu Arg Ile Glu Val Gln Pro	1248
	405 410 415	
10	AAG CCA CAT CAC CGG GCC CAC TAT GAG ACA GAA GGC AGC CGA GGG GCT Lys Pro His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg Gly Ala	1296
	420 425 430	
15	GTC AAA GCT CCA ACT GGA GGC CAC CCT GTG GTT CAG CTC CAT GGC TAC Val Lys Ala Pro Thr Gly Gly His Pro Val Val Gln Leu His Gly Tyr	1344
	435 440 445	
20	ATG GAA AAC AAG CCT CTG GGA CTT CAG ATC TTC ATT GGG ACA GCT GAT Met Glu Asn Lys Pro Leu Gly Leu Gln Ile Phe Ile Gly Thr Ala Asp	1392
	450 455 460	
25	GAG CGG ATC CTT AAG CCG CAC GCC TTC TAC CAG GTG CAC CGA ATC ACG Glu Arg Ile Leu Lys Pro His Ala Phe Tyr Gln Val His Arg Ile Thr	1440
	465 470 475 480	
30	GGG AAA ACT GTC ACC ACC ACC AGC TAT GAG AAG ATA GTG GGC AAC ACC Gly Lys Thr Val Thr Thr Thr Ser Tyr Glu Lys Ile Val Gly Asn Thr	1488
	485 490 495	
35	AAA GTC CTG GAG ATC CCC TTG GAG CCC AAA AAC AAC ATG AGG GCA ACC Lys Val Leu Glu Ile Pro Leu Glu Pro Lys Asn Asn Met Arg Ala Thr	1536
	500 505 510	
40	ATC GAC TGT GCG GGG ATC TTG AAG CTT AGA AAC GCC GAC ATT GAG CTG Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ala Asp Ile Glu Leu	1584
	515 520 525	
45	CGG AAA GGC GAG ACG GAC ATT GGA AGA AAG AAC ACG CGG GTG AGA CTG Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val Arg Leu	1632
	530 535 540	
50	GTT TTC CGA GTT CAC ATC CCA GAG TCC AGT GGC AGA ATC GTC TCT TTA Val Phe Arg Val His Ile Pro Glu Ser Ser Gly Arg Ile Val Ser Leu	1680
	545 550 555 560	
55	CAG ACT GCA TCT AAC CCC ATC GAG TGC TCC CAG CGA TCT GCT CAC GAG Gln Thr Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala His Glu	1728
	565 570 575	
60	CTG CCC ATG GTT GAA AGA CAA GAC ACA GAC AGC TGC CTG GTC TAT GGC Leu Pro Met Val Glu Arg Gln Asp Thr Asp Ser Cys Leu Val Tyr Gly	1776
	580 585 590	
65	GGC CAG CAA ATG ATC CTC ACG GGG CAG AAC TTT ACA TCC GAG TCC AAA Gly Gln Gln Met Ile Leu Thr Gly Gln Asn Phe Thr Ser Glu Ser Lys	1824
	595 600 605	
70	GTT GTG TTT ACT GAG AAG ACC ACA GAT GGA CAG CAA ATT TGG GAG ATG	1872

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	Val	Val	Phe	Thr	Glu	Lys	Thr	Thr	Asp	Gly	Gln	Gln	Ile	Trp	Glu	Met	
	610						615					620					
5	GAA	GCC	ACG	GTG	GAT	AAG	GAC	AAG	AGC	CAG	CCC	AAC	ATG	CTT	TTT	GTT	1920
	Glu	Ala	Thr	Val	Asp	Lys	Asp	Lys	Ser	Gln	Pro	Asn	Met	Leu	Phe	Val	
	625					630					635				640		
10	GAG	ATC	CCT	GAA	TAT	CGG	AAC	AAG	CAT	ATC	CGC	ACA	CCT	GTA	AAA	GTG	1968
	Glu	Ile	Pro	Glu	Tyr	Arg	Asn	Lys	His	Ile	Arg	Thr	Pro	Val	Lys	Val	
					645					650					655		
15	AAC	TTC	TAC	GTC	ATC	AAT	GGG	AAG	AGA	AAA	CGA	AGT	CAG	CCT	CAG	CAC	2016
	Asn	Phe	Tyr	Val	Ile	Asn	Gly	Lys	Arg	Lys	Arg	Ser	Gln	Pro	Gln	His	
				660					665					670			
20	TTT	ACC	TAC	CAC	CCA	GTC	CCA	GCC	ATC	AAG	ACG	GAG	CCC	ACG	GAT	GAA	2064
	Phe	Thr	Tyr	His	Pro	Val	Pro	Ala	Ile	Lys	Thr	Glu	Pro	Thr	Asp	Glu	
			675					680					685				
25	TAT	GAC	CCC	ACT	CTG	ATC	TGC	AGC	CCC	ACC	CAT	GGA	GGC	CTG	GGG	AGC	2112
	Tyr	Asp	Pro	Thr	Leu	Ile	Cys	Ser	Pro	Thr	His	Gly	Gly	Leu	Gly	Ser	
		690					695					700					
30	CAG	CCT	TAC	TAC	CCC	CAG	CAC	CCG	ATG	GTG	GCC	GAG	TCC	CCC	TCC	TGC	2160
	Gln	Pro	Tyr	Tyr	Pro	Gln	His	Pro	Met	Val	Ala	Glu	Ser	Pro	Ser	Cys	
	705					710					715					720	
35	CTC	GTG	GCC	ACC	ATG	GCT	CCC	TGC	CAG	CAG	TTC	CGC	ACG	GGG	CTC	TCA	2208
	Leu	Val	Ala	Thr	Met	Ala	Pro	Cys	Gln	Gln	Phe	Arg	Thr	Gly	Leu	Ser	
					725				730					735			
40	TCC	CCT	GAC	GCC	CGC	TAC	CAG	CAA	CAG	AAC	CCA	GCG	GCC	GTA	CTC	TAC	2256
	Ser	Pro	Asp	Ala	Arg	Tyr	Gln	Gln	Gln	Asn	Pro	Ala	Ala	Val	Leu	Tyr	
				740					745					750			
45	CAG	CGG	AGC	AAG	AGC	CTG	AGC	CCC	AGC	CTG	CTG	GGC	TAT	CAG	CAG	CCG	2304
	Gln	Arg	Ser	Lys	Ser	Leu	Ser	Pro	Ser	Leu	Leu	Gly	Tyr	Gln	Gln	Pro	
			755					760					765				
50	GCC	CTC	ATG	GCC	GCC	CCG	CTG	TCC	CTT	GCG	GAC	GCT	CAC	CGC	TCT	GTG	2352
	Ala	Leu	Met	Ala	Ala	Pro	Leu	Ser	Leu	Ala	Asp	Ala	His	Arg	Ser	Val	
		770					775					780					
55	CTG	GTG	CAC	GCC	GGC	TCC	CAG	GGC	CAG	AGC	TCA	GCC	CTG	CTC	CAC	CCC	2400
	Leu	Val	His	Ala	Gly	Ser	Gln	Gly	Gln	Ser	Ser	Ala	Leu	Leu	His	Pro	
	785					790					795					800	
60	TCT	CCG	ACC	AAC	CAG	CAG	GCC	TCG	CCT	GTG	ATC	CAC	TAC	TCA	CCC	ACC	2448
	Ser	Pro	Thr	Asn	Gln	Gln	Ala	Ser	Pro	Val	Ile	His	Tyr	Ser	Pro	Thr	
				805					810					815			
65	AAC	CAG	CAG	CTG	CGC	TGC	GGA	AGC	CAC	CAG	GAG	TTC	CAG	CAC	ATC	ATG	2496
	Asn	Gln	Gln	Leu	Arg	Cys	Gly	Ser	His	Gln	Glu	Phe	Gln	His	Ile	Met	
				820					825					830			
70	TAC	TGC	GAG	AAT	TTC	GCA	CCA	GGC	ACC	ACC	AGA	CCT	GGC	CCG	CCC	CCG	2544

264

265

	Tyr Cys Glu Asn Phe Ala Pro Gly Thr Thr Arg Pro Gly Pro Pro Pro	
	835 840 845	
5	GTC AGT CAA GGT CAG AGG CTG AGC CCG GGT TCC TAC CCC ACA GTC ATT Val Ser Gln Gly Gln Arg Leu Ser Pro Gly Ser Tyr Pro Thr Val Ile	2592
	850 855 860	
10	CAG CAG CAG AAT GCC ACG AGC CAA AGA GCC GCC AAA AAC GGA CCC CCG Gln Gln Gln Asn Ala Thr Ser Gln Arg Ala Ala Lys Asn Gly Pro Pro	2640
	865 870 875 880	
15	GTC AGT GAC CAA AAG GAA GTA TTA CCT GCG GGG GTG ACC ATT AAA CAG Val Ser Asp Gln Lys Glu Val Leu Pro Ala Gly Val Thr Ile Lys Gln	2688
	885 890 895	
	GAG CAG AAC TTG GAC CAG ACC TAC TTG GAT GAT GTT AAT GAA ATT ATC Glu Gln Asn Leu Asp Gln Thr Tyr Leu Asp Asp Val Asn Glu Ile Ile	2736
	900 905 910	
20	AGG AAG GAG TTT TCA GGA CCT CCT GCC AGA AAT CAG ACG AGA ATT CTG Arg Lys Glu Phe Ser Gly Pro Pro Ala Arg Asn Gln Thr Arg Ile Leu	2784
	915 920 925	
25	CAG TCG ACG GTA CCG CGG GCC CGG GAT CCA CCG GTC GCC ACC ATG GTG Gln Ser Thr Val Pro Arg Ala Arg Asp Pro Pro Val Ala Thr Met Val	2832
	930 935 940	
30	AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG GTC GAG Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu	2880
	945 950 955 960	
35	CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG GGC Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly	2928
	965 970 975	
	GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC TGC ACC Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr	2976
	980 985 990	
40	ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC CTG ACC Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr	3024
	995 1000 1005	
45	TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG CAG CAC Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His	3072
	1010 1015 1020	
50	GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG CGC ACC Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr	3120
	1025 1030 1035 1040	
55	ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG GTG AAG Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys	3168
	1045 1050 1055	
	TTC GAG GGC GAC ACC CTG GTG AAC CGC ATC GAG CTG AAG GGC ATC GAC	3216

265

266

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp  
1060 1065 1070

5 TTC AAG GAG GAC GGC AAC ATC CTG GGG CAC AAG CTG GAG TAC AAC TAC 3264  
Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr  
1075 1080 1085

10 AAC AGC CAC AAC GTC TAT ATC ATG GCC GAC AAG CAG AAG AAC GGC ATC 3312  
Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile  
1090 1095 1100

15 AAG GTG AAC TTC AAG ATC CGC CAC AAC ATC GAG GAC GGC AGC GTG CAG 3360  
Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln  
1105 1110 1115 1120

CTC GCC GAC CAC TAC CAG CAG AAC ACC CCC ATC GGC GAC GGC CCC GTG 3408  
Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val  
1125 1130 1135

20 CTG CTG CCC GAC AAC CAC TAC CTG AGC ACC CAG TCC GCC CTG AGC AAA 3456  
Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys  
1140 1145 1150

25 GAC CCC AAC GAG AAG CGC GAT CAC ATG GTC CTG CTG GAG TTC GTG ACC 3504  
Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr  
1155 1160 1165

GCC GCC GGG ATC ACT CTC GGC ATG GAC GAG CTG TAC AAG TAA 3546  
Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
30 1170 1175 1180

## (2) INFORMATION FOR SEQ ID NO:133:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1181 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- 40 (ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Met Asn Ala Pro Glu Arg Gln Pro Gln Pro Asp Gly Gly Asp Ala Pro  
1 5 10 15  
Gly His Glu Pro Gly Gly Ser Pro Gln Asp Glu Leu Asp Phe Ser Ile  
20 25 30  
50 Leu Phe Asp Tyr Glu Tyr Leu Asn Pro Asn Glu Glu Glu Pro Asn Ala  
35 40 45  
His Lys Val Ala Ser Pro Pro Ser Gly Pro Ala Tyr Pro Asp Asp Val  
50 55 60  
Met Asp Tyr Gly Leu Lys Pro Tyr Ser Pro Leu Ala Ser Leu Ser Gly  
55 65 70 75 80  
Glu Pro Pro Gly Arg Phe Gly Glu Pro Asp Arg Val Gly Pro Gln Lys

266

267

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		530					535					540						
		Val	Phe	Arg	Val	His	Ile	Pro	Glu	Ser	Ser	Gly	Arg	Ile	Val	Ser	Leu	
		545					550					555					560	
5		Gln	Thr	Ala	Ser	Asn	Pro	Ile	Glu	Cys	Ser	Gln	Arg	Ser	Ala	His	Glu	
						565						570					575	
		Leu	Pro	Met	Val	Glu	Arg	Gln	Asp	Thr	Asp	Ser	Cys	Leu	Val	Tyr	Gly	
					580						585					590		
		Gly	Gln	Gln	Met	Ile	Leu	Thr	Gly	Gln	Asn	Phe	Thr	Ser	Glu	Ser	Lys	
					595				600					605				
10		Val	Val	Phe	Thr	Glu	Lys	Thr	Thr	Asp	Gly	Gln	Gln	Ile	Trp	Glu	Met	
			610					615					620					
		Glu	Ala	Thr	Val	Asp	Lys	Asp	Lys	Ser	Gln	Pro	Asn	Met	Leu	Phe	Val	
			625				630					635					640	
		Glu	Ile	Pro	Glu	Tyr	Arg	Asn	Lys	His	Ile	Arg	Thr	Pro	Val	Lys	Val	
15						645						650					655	
		Asn	Phe	Tyr	Val	Ile	Asn	Gly	Lys	Arg	Lys	Arg	Ser	Gln	Pro	Gln	His	
					660						665					670		
		Phe	Thr	Tyr	His	Pro	Val	Pro	Ala	Ile	Lys	Thr	Glu	Pro	Thr	Asp	Glu	
					675					680					685			
20		Tyr	Asp	Pro	Thr	Leu	Ile	Cys	Ser	Pro	Thr	His	Gly	Gly	Leu	Gly	Ser	
			690					695					700					
		Gln	Pro	Tyr	Tyr	Pro	Gln	His	Pro	Met	Val	Ala	Glu	Ser	Pro	Ser	Cys	
						710						715					720	
25		Leu	Val	Ala	Thr	Met	Ala	Pro	Cys	Gln	Gln	Phe	Arg	Thr	Gly	Leu	Ser	
						725						730					735	
		Ser	Pro	Asp	Ala	Arg	Tyr	Gln	Gln	Gln	Asn	Pro	Ala	Ala	Val	Leu	Tyr	
					740					745					750			
		Gln	Arg	Ser	Lys	Ser	Leu	Ser	Pro	Ser	Leu	Leu	Gly	Tyr	Gln	Gln	Pro	
					755				760					765				
30		Ala	Leu	Met	Ala	Ala	Pro	Leu	Ser	Leu	Ala	Asp	Ala	His	Arg	Ser	Val	
			770					775					780					
		Leu	Val	His	Ala	Gly	Ser	Gln	Gly	Gln	Ser	Ser	Ala	Leu	Leu	His	Pro	
						790						795					800	
35		Ser	Pro	Thr	Asn	Gln	Gln	Ala	Ser	Pro	Val	Ile	His	Tyr	Ser	Pro	Thr	
						805						810					815	
		Asn	Gln	Gln	Leu	Arg	Cys	Gly	Ser	His	Gln	Glu	Phe	Gln	His	Ile	Met	
					820						825				830			
		Tyr	Cys	Glu	Asn	Phe	Ala	Pro	Gly	Thr	Thr	Arg	Pro	Gly	Pro	Pro	Pro	
					835				840					845				
40		Val	Ser	Gln	Gly	Gln	Arg	Leu	Ser	Pro	Gly	Ser	Tyr	Pro	Thr	Val	Ile	
			850					855					860					
		Gln	Gln	Gln	Asn	Ala	Thr	Ser	Gln	Arg	Ala	Ala	Lys	Asn	Gly	Pro	Pro	
						870						875					880	
45		Val	Ser	Asp	Gln	Lys	Glu	Val	Leu	Pro	Ala	Gly	Val	Thr	Ile	Lys	Gln	
						885						890					895	
		Glu	Gln	Asn	Leu	Asp	Gln	Thr	Tyr	Leu	Asp	Asp	Val	Asn	Glu	Ile	Ile	
					900					905				910				
		Arg	Lys	Glu	Phe	Ser	Gly	Pro	Pro	Ala	Arg	Asn	Gln	Thr	Arg	Ile	Leu	
					915				920					925				
50		Gln	Ser	Thr	Val	Pro	Arg	Ala	Arg	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	
			930					935					940					
		Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	
						950						955					960	
55		Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	
						965						970					975	
		Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	

268



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	980								985				990							
	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr				
	995				1000				1005											
5	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His				
	1010				1015				1020											
	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr				
	025	1030				1035				1040										
	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys				
	1045				1050				1055											
10	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp				
	1060				1065				1070											
	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr				
	1075				1080				1085											
	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile				
15	1090				1095				1100											
	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln				
	105	1110				1115				1120										
	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val				
	1125				1130				1135											
20	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys				
	1140				1145				1150											
	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr				
	1155				1160				1165											
	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys							
25	1170				1175				1180											

(2) INFORMATION FOR SEO ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 2802 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

40 (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...2799  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

45	ATG Met 1	GTG Val	AGC Ser	AAG Lys	GGC Gly 5	GAG Glu	GAG Glu	CTG Leu	TTC Phe	ACC Thr	GGG Gly	GTG Val	GTG Val	CCC Pro	ATC Ile	CTG Leu	48
50	GTC Val	GAG Glu	CTG Leu	GAC Asp 20	GGC Gly	GAC Asp	GTA Val	AAC Asn	GGC Gly 25	CAC His	AAG Lys	TTC Phe	AGC Ser	GTG Val	TCC Ser	GGC Gly	96
55	GAG Glu	GGC Gly	GAG Glu	GGC Gly	GAT Asp	GCC Ala	ACC Thr	TAC Tyr 40	GGC Gly	AAG Lys	CTG Leu	ACC Thr	CTG Leu	AAG Lys	TTC Phe	ATC Ile	144
	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	192

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	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50						55					60					
5	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	240
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70				75						80	
10	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	288
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85					90					95		
15	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
20	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115						120					125				
25	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130					135					140					
30	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150				155						160	
35	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165					170						175		
40	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180				185					190				
45	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
		195						200					205				
50	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215					220					
55	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230				235						240	
60	GGA	CTC	AGA	TCT	CGA	GGG	AGC	ATG	GGC	ACC	TTG	CGG	GAT	TTA	CAG	TAC	768
	Gly	Leu	Arg	Ser	Arg	Gly	Ser	Met	Gly	Thr	Leu	Arg	Asp	Leu	Gln	Tyr	
				245					250						255		
65	GCG	CTC	CAG	GAG	AAG	ATC	GAG	GAG	CTG	AGG	CAG	CGG	GAT	GCT	CTC	ATC	816
	Ala	Leu	Gln	Glu	Lys	Ile	Glu	Glu	Leu	Arg	Gln	Arg	Asp	Ala	Leu	Ile	
				260					265					270			
70	GAC	GAG	CTG	GAG	CTG	GAG	TTG	GAT	CAG	AAG	GAC	GAA	CTG	ATC	CAG	AAG	864

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	Asp	Glu	Leu	Glu	Leu	Glu	Leu	Asp	Gln	Lys	Asp	Glu	Leu	Ile	Gln	Lys	
			275					280					285				
5	CTG	CAG	AAC	GAG	CTG	GAC	AAG	TAC	CGC	TCG	GTG	ATC	CGA	CCA	GCC	ACC	912
	Leu	Gln	Asn	Glu	Leu	Asp	Lys	Tyr	Arg	Ser	Val	Ile	Arg	Pro	Ala	Thr	
			290				295					300					
10	CAG	CAG	GCG	CAG	AAG	CAG	AGC	GCG	AGC	ACC	TTG	CAG	GGC	GAG	CCG	CGC	960
	Gln	Gln	Ala	Gln	Lys	Gln	Ser	Ala	Ser	Thr	Leu	Gln	Gly	Glu	Pro	Arg	
			305			310					315					320	
15	ACC	AAG	CGG	CAG	GCG	ATC	TCC	GCC	GAG	CCC	ACC	GCC	TTC	GAC	ATC	CAG	1008
	Thr	Lys	Arg	Gln	Ala	Ile	Ser	Ala	Glu	Pro	Thr	Ala	Phe	Asp	Ile	Gln	
				325					330						335		
	GAT	CTC	AGC	CAT	GTG	ACC	CTG	CCC	TTC	TAC	CCC	AAG	AGC	CCA	CAG	TCC	1056
	Asp	Leu	Ser	His	Val	Thr	Leu	Pro	Phe	Tyr	Pro	Lys	Ser	Pro	Gln	Ser	
				340					345					350			
20	AAG	GAT	CTT	ATA	AAG	GAA	GCT	ATC	CTT	GAC	AAT	GAC	TTT	ATG	AAG	AAC	1104
	Lys	Asp	Leu	Ile	Lys	Glu	Ala	Ile	Leu	Asp	Asn	Asp	Phe	Met	Lys	Asn	
			355				360						365				
25	TTG	GAG	CTG	TCG	CAG	ATC	CAG	GAG	ATT	GTG	GAT	TGT	ATG	TAC	CCG	GTG	1152
	Leu	Glu	Leu	Ser	Gln	Ile	Gln	Glu	Ile	Val	Asp	Cys	Met	Tyr	Pro	Val	
			370				375					380					
30	GAG	TAT	GCG	AAG	GAC	AGT	TGC	ATC	ATC	AAA	GAA	GGA	GAC	GTG	GGG	TCA	1200
	Glu	Tyr	Gly	Lys	Asp	Ser	Cys	Ile	Ile	Lys	Glu	Gly	Asp	Val	Gly	Ser	
			385			390					395					400	
35	CTG	GTG	TAT	GTC	ATG	GAA	GAT	GGT	AAG	GTT	GAA	GTT	ACA	AAA	GAA	GGT	1248
	Leu	Val	Tyr	Val	Met	Glu	Asp	Gly	Lys	Val	Glu	Val	Thr	Lys	Glu	Gly	
				405					410						415		
	GTG	AAG	TTG	TGT	ACC	ATG	GGT	CCA	GGA	AAA	GTG	TTT	GGG	GAA	TTG	GCT	1296
	Val	Lys	Leu	Cys	Thr	Met	Gly	Pro	Gly	Lys	Val	Phe	Gly	Glu	Leu	Ala	
				420					425					430			
40	ATT	CTT	TAC	AAC	TGT	ACC	CGG	ACA	GCG	ACC	GTC	AAG	ACT	CTT	GTA	AAT	1344
	Ile	Leu	Tyr	Asn	Cys	Thr	Arg	Thr	Ala	Thr	Val	Lys	Thr	Leu	Val	Asn	
			435					440					445				
45	GTA	AAA	CTC	TGG	GCC	ATT	GAT	CGA	CAA	TGT	TTT	CAA	ACA	ATA	ATG	ATG	1392
	Val	Lys	Leu	Trp	Ala	Ile	Asp	Arg	Gln	Cys	Phe	Gln	Thr	Ile	Met	Met	
			450				455					460					
50	AGG	ACA	GGA	CTC	ATC	AAG	CAT	ACC	GAG	TAT	ATG	GAA	TTT	TTA	AAA	AGC	1440
	Arg	Thr	Gly	Leu	Ile	Lys	His	Thr	Glu	Tyr	Met	Glu	Phe	Leu	Lys	Ser	
			465			470				475						480	
55	GTT	CCA	ACA	TTC	CAG	AGC	CTT	CCT	GAA	GAG	ATC	CTC	AGC	AAG	CTT	GCT	1488
	Val	Pro	Thr	Phe	Gln	Ser	Leu	Pro	Glu	Glu	Ile	Leu	Ser	Lys	Leu	Ala	
				485					490						495		
	GAT	GTC	CTT	GAA	GAG	ACC	CAC	TAT	GAA	AAT	GGA	GAA	TAT	ATT	ATC	AGG	1536

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	Asp	Val	Leu	Glu	Glu	Thr	His	Tyr	Glu	Asn	Gly	Glu	Tyr	Ile	Ile	Arg	
				500					505					510			
5	CAA	GGT	GCA	AGA	GGG	GAC	ACC	TTC	TTT	ATC	ATC	AGC	AAA	GGA	ACG	GTA	1584
	Gln	Gly	Ala	Arg	Gly	Asp	Thr	Phe	Phe	Ile	Ile	Ser	Lys	Gly	Thr	Val	
			515				520					525					
10	AAT	GTC	ACT	CGT	GAA	GAC	TCA	CCG	AGT	GAA	GAC	CCA	GTC	TTT	CTT	AGA	1632
	Asn	Val	Thr	Arg	Glu	Asp	Ser	Pro	Ser	Glu	Asp	Pro	Val	Phe	Leu	Arg	
		530					535					540					
15	ACT	TTA	GGA	AAA	GGA	GAC	TGG	TTT	GGA	GAG	AAA	GCC	TTG	CAG	GGG	GAA	1680
	Thr	Leu	Gly	Lys	Gly	Asp	Trp	Phe	Gly	Glu	Lys	Ala	Leu	Gln	Gly	Glu	
	545				550					555					560		
	GAT	GTG	AGA	ACA	GCA	AAC	GTA	ATT	GCT	GCA	GAA	GCT	GTA	ACC	TGC	CTT	1728
	Asp	Val	Arg	Thr	Ala	Asn	Val	Ile	Ala	Ala	Glu	Ala	Val	Thr	Cys	Leu	
					565				570						575		
20	GTG	ATT	GAC	AGA	GAC	TCT	TTT	AAA	CAT	TTG	ATT	GGA	GGG	CTG	GAT	GAT	1776
	Val	Ile	Asp	Arg	Asp	Ser	Phe	Lys	His	Leu	Ile	Gly	Gly	Leu	Asp	Asp	
				580				585						590			
25	GTT	TCT	AAT	AAA	GCA	TAT	GAA	GAT	GCA	GAA	GCT	AAA	GCA	AAA	TAT	GAA	1824
	Val	Ser	Asn	Lys	Ala	Tyr	Glu	Asp	Ala	Glu	Ala	Lys	Ala	Lys	Tyr	Glu	
			595				600					605					
30	GCT	GAA	GCG	GCT	TTC	TTC	GCC	AAC	CTG	AAG	CTG	TCT	GAT	TTC	AAC	ATC	1872
	Ala	Glu	Ala	Ala	Phe	Phe	Ala	Asn	Leu	Lys	Leu	Ser	Asp	Phe	Asn	Ile	
		610					615					620					
35	ATT	GAT	ACC	CTT	GGA	GTT	GGA	GGT	TTC	GGA	CGA	GTA	GAA	CTG	GTC	CAG	1920
	Ile	Asp	Thr	Leu	Gly	Val	Gly	Gly	Phe	Gly	Arg	Val	Glu	Leu	Val	Gln	
	625				630					635					640		
	TTG	AAA	AGT	GAA	GAA	TCC	AAA	ACG	TTT	GCA	ATG	AAG	ATT	CTC	AAG	AAA	1968
	Leu	Lys	Ser	Glu	Glu	Ser	Lys	Thr	Phe	Ala	Met	Lys	Ile	Leu	Lys	Lys	
					645				650					655			
40	CGT	CAC	ATT	GTG	GAC	ACA	AGA	CAG	CAG	GAG	CAC	ATC	CGC	TCA	GAG	AAG	2016
	Arg	His	Ile	Val	Asp	Thr	Arg	Gln	Gln	Glu	His	Ile	Arg	Ser	Glu	Lys	
				660				665					670				
45	CAG	ATC	ATG	CAG	GGG	GCT	CAT	TCC	GAT	TTC	ATA	GTG	AGA	CTG	TAC	AGA	2064
	Gln	Ile	Met	Gln	Gly	Ala	His	Ser	Asp	Phe	Ile	Val	Arg	Leu	Tyr	Arg	
			675				680					685					
50	ACA	TTT	AAG	GAC	AGC	AAA	TAT	TTG	TAT	ATG	TTG	ATG	GAA	GCT	TGT	CTA	2112
	Thr	Phe	Lys	Asp	Ser	Lys	Tyr	Leu	Tyr	Met	Leu	Met	Glu	Ala	Cys	Leu	
		690					695				700						
55	GGT	GGA	GAG	CTC	TGG	ACC	ATT	CTC	AGG	GAT	AGA	GGT	TCG	TTT	GAA	GAT	2160
	Gly	Gly	Glu	Leu	Trp	Thr	Ile	Leu	Arg	Asp	Arg	Gly	Ser	Phe	Glu	Asp	
	705				710					715					720		
	TCT	ACA	ACC	AGA	TTT	TAC	ACA	GCA	TGT	GTG	GTA	GAA	GCT	TTT	GCC	TAT	2208

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	Ser	Thr	Thr	Arg	Phe	Tyr	Thr	Ala	Cys	Val	Val	Glu	Ala	Phe	Ala	Tyr	
					725					730					735		
5	CTG	CAT	TCC	AAA	GGA	ATC	ATT	TAC	AGG	GAC	CTC	AAG	CCA	GAA	AAT	CTC	2256
	Leu	His	Ser	Lys	Gly	Ile	Ile	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	
				740					745					750			
10	ATC	CTA	GAT	CAC	CGA	GGT	TAT	GCC	AAA	CTG	GTT	GAT	TTT	GGC	TTT	GCA	2304
	Ile	Leu	Asp	His	Arg	Gly	Tyr	Ala	Lys	Leu	Val	Asp	Phe	Gly	Phe	Ala	
				755				760						765			
15	AAG	AAA	ATA	GGA	TTT	GGA	AAG	AAA	ACA	TGG	ACT	TTT	TGT	GGG	ACT	CCA	2352
	Lys	Lys	Ile	Gly	Phe	Gly	Lys	Lys	Thr	Trp	Thr	Phe	Cys	Gly	Thr	Pro	
				770				775						780			
	GAG	TAT	GTA	GCC	CCA	GAG	ATC	ATC	CTG	AAC	AAA	GGC	CAT	GAC	ATT	TCA	2400
	Glu	Tyr	Val	Ala	Pro	Glu	Ile	Ile	Leu	Asn	Lys	Gly	His	Asp	Ile	Ser	
						790						795				800	
20	GCC	GAC	TAC	TGG	TCA	CTG	GGA	ATC	CTA	ATG	TAT	GAA	CTC	CTG	ACT	GGC	2448
	Ala	Asp	Tyr	Trp	Ser	Leu	Gly	Ile	Leu	Met	Tyr	Glu	Leu	Leu	Thr	Gly	
					805					810					815		
25	AGC	CCA	CCT	TTC	TCA	GGC	CCA	GAT	CCT	ATG	AAA	ACC	TAT	AAC	ATC	ATA	2496
	Ser	Pro	Pro	Phe	Ser	Gly	Pro	Asp	Pro	Met	Lys	Thr	Tyr	Asn	Ile	Ile	
				820					825						830		
30	TTG	AGG	GGG	ATT	GAC	ATG	ATA	GAA	TTT	CCA	AAG	AAG	ATT	GCC	AAA	AAT	2544
	Leu	Arg	Gly	Ile	Asp	Met	Ile	Glu	Phe	Pro	Lys	Lys	Ile	Ala	Lys	Asn	
				835				840						845			
35	GCT	GCT	AAT	TTA	ATT	AAA	AAA	CTA	TGC	AGG	GAC	AAT	CCA	TCA	GAA	AGA	2592
	Ala	Ala	Asn	Leu	Ile	Lys	Lys	Leu	Cys	Arg	Asp	Asn	Pro	Ser	Glu	Arg	
				850				855						860			
	TTA	GGG	AAT	TTG	AAA	AAT	GGA	GTA	AAA	GAC	ATT	CAA	AAG	CAC	AAA	TGG	2640
	Leu	Gly	Asn	Leu	Lys	Asn	Gly	Val	Lys	Asp	Ile	Gln	Lys	His	Lys	Trp	
				865			870				875					880	
40	TTT	GAG	GGC	TTT	AAC	TGG	GAA	GGC	TTA	AGA	AAA	GGT	ACC	TTG	ACA	CCT	2688
	Phe	Glu	Gly	Phe	Asn	Trp	Glu	Gly	Leu	Arg	Lys	Gly	Thr	Leu	Thr	Pro	
					885					890					895		
45	CCT	ATA	ATA	CCA	AGT	GTT	GCA	TCA	CCC	ACA	GAC	ACA	AGT	AAT	TTT	GAC	2736
	Pro	Ile	Ile	Pro	Ser	Val	Ala	Ser	Pro	Thr	Asp	Thr	Ser	Asn	Phe	Asp	
				900					905						910		
50	AGT	TTC	CCT	GAG	GAC	AAC	GAT	GAA	CCA	CCA	CCT	GAT	GAC	AAC	TCA	GGA	2784
	Ser	Phe	Pro	Glu	Asp	Asn	Asp	Glu	Pro	Pro	Pro	Asp	Asp	Asn	Ser	Gly	
				915				920						925			
55	TGG	GAT	ATA	GAC	TTC	TAA											2802
	Trp	Asp	Ile	Asp	Phe												
				930													

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## (2) INFORMATION FOR SEQ ID NO:135:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 933 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

- 10 (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

15 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
 1 5 10 15  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 20 25 30  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 20 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 25 85 90 95  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 30 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 35 165 170 175  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190  
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
 195 200 205  
 40 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220  
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser  
 225 230 235 240  
 Gly Leu Arg Ser Arg Gly Ser Met Gly Thr Leu Arg Asp Leu Gln Tyr  
 45 245 250 255  
 Ala Leu Gln Glu Lys Ile Glu Glu Leu Arg Gln Arg Asp Ala Leu Ile  
 260 265 270  
 Asp Glu Leu Glu Leu Glu Leu Asp Gln Lys Asp Glu Leu Ile Gln Lys  
 275 280 285  
 50 Leu Gln Asn Glu Leu Asp Lys Tyr Arg Ser Val Ile Arg Pro Ala Thr  
 290 295 300  
 Gln Gln Ala Gln Lys Gln Ser Ala Ser Thr Leu Gln Gly Glu Pro Arg  
 305 310 315 320  
 Thr Lys Arg Gln Ala Ile Ser Ala Glu Pro Thr Ala Phe Asp Ile Gln  
 55 325 330 335  
 Asp Leu Ser His Val Thr Leu Pro Phe Tyr Pro Lys Ser Pro Gln Ser

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			340				345				350					
	Lys	Asp	Leu	Ile	Lys	Glu	Ala	Ile	Leu	Asp	Asn	Asp	Phe	Met	Lys	Asn
			355					360					365			
5	Leu	Glu	Leu	Ser	Gln	Ile	Gln	Glu	Ile	Val	Asp	Cys	Met	Tyr	Pro	Val
			370				375					380				
	Glu	Tyr	Gly	Lys	Asp	Ser	Cys	Ile	Ile	Lys	Glu	Gly	Asp	Val	Gly	Ser
	385					390					395					400
	Leu	Val	Tyr	Val	Met	Glu	Asp	Gly	Lys	Val	Glu	Val	Thr	Lys	Glu	Gly
					405					410					415	
10	Val	Lys	Leu	Cys	Thr	Met	Gly	Pro	Gly	Lys	Val	Phe	Gly	Glu	Leu	Ala
				420					425					430		
	Ile	Leu	Tyr	Asn	Cys	Thr	Arg	Thr	Ala	Thr	Val	Lys	Thr	Leu	Val	Asn
			435					440					445			
	Val	Lys	Leu	Trp	Ala	Ile	Asp	Arg	Gln	Cys	Phe	Gln	Thr	Ile	Met	Met
15			450				455					460				
	Arg	Thr	Gly	Leu	Ile	Lys	His	Thr	Glu	Tyr	Met	Glu	Phe	Leu	Lys	Ser
	465					470					475					480
	Val	Pro	Thr	Phe	Gln	Ser	Leu	Pro	Glu	Glu	Ile	Leu	Ser	Lys	Leu	Ala
					485					490					495	
20	Asp	Val	Leu	Glu	Glu	Thr	His	Tyr	Glu	Asn	Gly	Glu	Tyr	Ile	Ile	Arg
				500					505					510		
	Gln	Gly	Ala	Arg	Gly	Asp	Thr	Phe	Phe	Ile	Ile	Ser	Lys	Gly	Thr	Val
			515					520					525			
	Asn	Val	Thr	Arg	Glu	Asp	Ser	Pro	Ser	Glu	Asp	Pro	Val	Phe	Leu	Arg
25			530				535					540				
	Thr	Leu	Gly	Lys	Gly	Asp	Trp	Phe	Gly	Glu	Lys	Ala	Leu	Gln	Gly	Glu
	545					550					555					560
	Asp	Val	Arg	Thr	Ala	Asn	Val	Ile	Ala	Ala	Glu	Ala	Val	Thr	Cys	Leu
					565					570					575	
30	Val	Ile	Asp	Arg	Asp	Ser	Phe	Lys	His	Leu	Ile	Gly	Gly	Leu	Asp	Asp
				580					585					590		
	Val	Ser	Asn	Lys	Ala	Tyr	Glu	Asp	Ala	Glu	Ala	Lys	Ala	Lys	Tyr	Glu
			595					600					605			
	Ala	Glu	Ala	Ala	Phe	Phe	Ala	Asn	Leu	Lys	Leu	Ser	Asp	Phe	Asn	Ile
35			610				615					620				
	Ile	Asp	Thr	Leu	Gly	Val	Gly	Gly	Phe	Gly	Arg	Val	Glu	Leu	Val	Gln
	625					630					635					640
	Leu	Lys	Ser	Glu	Glu	Ser	Lys	Thr	Phe	Ala	Met	Lys	Ile	Leu	Lys	Lys
					645					650					655	
40	Arg	His	Ile	Val	Asp	Thr	Arg	Gln	Gln	Glu	His	Ile	Arg	Ser	Glu	Lys
				660					665					670		
	Gln	Ile	Met	Gln	Gly	Ala	His	Ser	Asp	Phe	Ile	Val	Arg	Leu	Tyr	Arg
			675					680					685			
	Thr	Phe	Lys	Asp	Ser	Lys	Tyr	Leu	Tyr	Met	Leu	Met	Glu	Ala	Cys	Leu
45			690				695					700				
	Gly	Gly	Glu	Leu	Trp	Thr	Ile	Leu	Arg	Asp	Arg	Gly	Ser	Phe	Glu	Asp
	705					710					715					720
	Ser	Thr	Thr	Arg	Phe	Tyr	Thr	Ala	Cys	Val	Val	Glu	Ala	Phe	Ala	Tyr
					725					730					735	
50	Leu	His	Ser	Lys	Gly	Ile	Ile	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu
				740					745					750		
	Ile	Leu	Asp	His	Arg	Gly	Tyr	Ala	Lys	Leu	Val	Asp	Phe	Gly	Phe	Ala
			755					760					765			
	Lys	Lys	Ile	Gly	Phe	Gly	Lys	Lys	Thr	Trp	Thr	Phe	Cys	Gly	Thr	Pro
55			770				775					780				
	Glu	Tyr	Val	Ala	Pro	Glu	Ile	Ile	Leu	Asn	Lys	Gly	His	Asp	Ile	Ser

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[illegible]

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2799 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...2795  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

	ATG	GGC	ACC	TTG	CGG	GAT	TTA	CAG	TAC	GCG	CTC	CAG	GAG	AAG	ATC	GAG	48
	Met	Gly	Thr	Leu	Arg	Asp	Leu	Gln	Tyr	Ala	Leu	Gln	Glu	Lys	Ile	Glu	
40	1				5					10					15		
	GAG	CTG	AGG	CAG	CGG	GAT	GCT	CTC	ATC	GAC	GAG	CTG	GAG	CTG	GAG	TTG	96
	Glu	Leu	Arg	Gln	Arg	Asp	Ala	Leu	Ile	Asp	Glu	Leu	Glu	Leu	Glu	Leu	
				20					25					30			
45	GAT	CAG	AAG	GAC	GAA	CTG	ATC	CAG	AAG	CTG	CAG	AAC	GAG	CTG	GAC	AAG	144
	Asp	Gln	Lys	Asp	Glu	Leu	Ile	Gln	Lys	Leu	Gln	Asn	Glu	Leu	Asp	Lys	
			35					40					45				
50	TAC	CGC	TCG	GTG	ATC	CGA	CCA	GCC	ACC	CAG	CAG	GCG	CAG	AAG	CAG	AGC	192
	Tyr	Arg	Ser	Val	Ile	Arg	Pro	Ala	Thr	Gln	Gln	Ala	Gln	Lys	Gln	Ser	
		50					55					60					
	GCG	AGC	ACC	TTG	CAG	GGC	GAG	CCG	CGC	ACC	AAG	CGG	CAG	GCG	ATC	TCC	240
55	Ala	Ser	Thr	Leu	Gln	Gly	Glu	Pro	Arg	Thr	Lys	Arg	Gln	Ala	Ile	Ser	
	65					70					75					80	



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	GCC GAG CCC ACC GCC TTC GAC ATC CAG GAT CTC AGC CAT GTG ACC CTG	288
	Ala Glu Pro Thr Ala Phe Asp Ile Gln Asp Leu Ser His Val Thr Leu	
	85 90 95	
5	CCC TTC TAC CCC AAG AGC CCA CAG TCC AAG GAT CTT ATA AAG GAA GCT	336
	Pro Phe Tyr Pro Lys Ser Pro Gln Ser Lys Asp Leu Ile Lys Glu Ala	
	100 105 110	
10	ATC CTT GAC AAT GAC TTT ATG AAG AAC TTG GAG CTG TCG CAG ATC CAG	384
	Ile Leu Asp Asn Asp Phe Met Lys Asn Leu Glu Leu Ser Gln Ile Gln	
	115 120 125	
15	GAG ATT GTG GAT TGT ATG TAC CCG GTG GAG TAT GGC AAG GAC AGT TGC	432
	Glu Ile Val Asp Cys Met Tyr Pro Val Glu Tyr Gly Lys Asp Ser Cys	
	130 135 140	
20	ATC ATC AAA GAA GGA GAC GTG GGG TCA CTG GTG TAT GTC ATG GAA GAT	480
	Ile Ile Lys Glu Gly Asp Val Gly Ser Leu Val Tyr Val Met Glu Asp	
	145 150 155 160	
	GGT AAG GTT GAA GTT ACA AAA GAA GGT GTG AAG TTG TGT ACC ATG GGT	528
	Gly Lys Val Glu Val Thr Lys Glu Gly Val Lys Leu Cys Thr Met Gly	
	165 170 175	
25	CCA GGA AAA GTG TTT GGG GAA TTG GCT ATT CTT TAC AAC TGT ACC CGG	576
	Pro Gly Lys Val Phe Gly Glu Leu Ala Ile Leu Tyr Asn Cys Thr Arg	
	180 185 190	
30	ACA GCG ACC GTC AAG ACT CTT GTA AAT GTA AAA CTC TGG GCC ATT GAT	624
	Thr Ala Thr Val Lys Thr Leu Val Asn Val Lys Leu Trp Ala Ile Asp	
	195 200 205	
35	CGA CAA TGT TTT CAA ACA ATA ATG ATG AGG ACA GGA CTC ATC AAG CAT	672
	Arg Gln Cys Phe Gln Thr Ile Met Met Arg Thr Gly Leu Ile Lys His	
	210 215 220	
40	ACC GAG TAT ATG GAA TTT TTA AAA AGC GTT CCA ACA TTC CAG AGC CTT	720
	Thr Glu Tyr Met Glu Phe Leu Lys Ser Val Pro Thr Phe Gln Ser Leu	
	225 230 235 240	
	CCT GAA GAG ATC CTC AGC AAG CTT GCT GAT GTC CTT GAA GAG ACC CAC	768
	Pro Glu Glu Ile Leu Ser Lys Leu Ala Asp Val Leu Glu Glu Thr His	
	245 250 255	
45	TAT GAA AAT GGA GAA TAT ATT ATC AGG CAA GGT GCA AGA GGG GAC ACC	816
	Tyr Glu Asn Gly Glu Tyr Ile Ile Arg Gln Gly Ala Arg Gly Asp Thr	
	260 265 270	
50	TTC TTT ATC ATC AGC AAA GGA ACG GTA AAT GTC ACT CGT GAA GAC TCA	864
	Phe Phe Ile Ile Ser Lys Gly Thr Val Asn Val Thr Arg Glu Asp Ser	
	275 280 285	
55	CCG AGT GAA GAC CCA GTC TTT CTT AGA ACT TTA GGA AAA GGA GAC TGG	912
	Pro Ser Glu Asp Pro Val Phe Leu Arg Thr Leu Gly Lys Gly Asp Trp	
	290 295 300	

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5	TTT GGA GAG AAA GCC TTG CAG GGG GAA GAT GTG AGA ACA GCA AAC GTA	960
	Phe Gly Glu Lys Ala Leu Gln Gly Glu Asp Val Arg Thr Ala Asn Val	
	305 310 315 320	
10	ATT GCT GCA GAA GCT GTA ACC TGC CTT GTG ATT GAC AGA GAC TCT TTT	1008
	Ile Ala Ala Glu Ala Val Thr Cys Leu Val Ile Asp Arg Asp Ser Phe	
	325 330 335	
15	AAA CAT TTG ATT GGA GGG CTG GAT GAT GTT TCT AAT AAA GCA TAT GAA	1056
	Lys His Leu Ile Gly Gly Leu Asp Asp Val Ser Asn Lys Ala Tyr Glu	
	340 345 350	
20	GAT GCA GAA GCT AAA GCA AAA TAT GAA GCT GAA GCG GCT TTC TTC GCC	1104
	Asp Ala Glu Ala Lys Ala Lys Tyr Glu Ala Glu Ala Ala Phe Phe Ala	
	355 360 365	
25	AAC CTG AAG CTG TCT GAT TTC AAC ATC ATT GAT ACC CTT GGA GTT GGA	1152
	Asn Leu Lys Leu Ser Asp Phe Asn Ile Ile Asp Thr Leu Gly Val Gly	
	370 375 380	
30	GGT TTC GGA CGA GTA GAA CTG GTC CAG TTG AAA AGT GAA GAA TCC AAA	1200
	Gly Phe Gly Arg Val Glu Leu Val Gln Leu Lys Ser Glu Glu Ser Lys	
	385 390 395 400	
35	ACG TTT GCA ATG AAG ATT CTC AAG AAA CGT CAC ATT GTG GAC ACA AGA	1248
	Thr Phe Ala Met Lys Ile Leu Lys Lys Arg His Ile Val Asp Thr Arg	
	405 410 415	
40	CAG CAG GAG CAC ATC CGC TCA GAG AAG CAG ATC ATG CAG GGG GCT CAT	1296
	Gln Gln Glu His Ile Arg Ser Glu Lys Gln Ile Met Gln Gly Ala His	
	420 425 430	
45	TCC GAT TTC ATA GTG AGA CTG TAC AGA ACA TTT AAG GAC AGC AAA TAT	1344
	Ser Asp Phe Ile Val Arg Leu Tyr Arg Thr Phe Lys Asp Ser Lys Tyr	
	435 440 445	
50	TTG TAT ATG TTG ATG GAA GCT TGT CTA GGT GGA GAG CTC TGG ACC ATT	1392
	Leu Tyr Met Leu Met Glu Ala Cys Leu Gly Gly Glu Leu Trp Thr Ile	
	450 455 460	
55	CTC AGG GAT AGA GGT TCG TTT GAA GAT TCT ACA ACC AGA TTT TAC ACA	1440
	Leu Arg Asp Arg Gly Ser Phe Glu Asp Ser Thr Thr Arg Phe Tyr Thr	
	465 470 475 480	
60	GCA TGT GTG GTA GAA GCT TTT GCC TAT CTG CAT TCC AAA GGA ATC ATT	1488
	Ala Cys Val Val Glu Ala Phe Ala Tyr Leu His Ser Lys Gly Ile Ile	
	485 490 495	
65	TAC AGG GAC CTC AAG CCA GAA AAT CTC ATC CTA GAT CAC CGA GGT TAT	1536
	Tyr Arg Asp Leu Lys Pro Glu Asn Leu Ile Leu Asp His Arg Gly Tyr	
	500 505 510	
70	GCC AAA CTG GTT GAT TTT GGC TTT GCA AAG AAA ATA GGA TTT GGA AAG	1584
	Ala Lys Leu Val Asp Phe Gly Phe Ala Lys Lys Ile Gly Phe Gly Lys	
	515 520 525	

278

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5	AAA ACA TGG ACT TTT TGT GGG ACT CCA GAG TAT GTA GCC CCA GAG ATC	1632
	Lys Thr Trp Thr Phe Cys Gly Thr Pro Glu Tyr Val Ala Pro Glu Ile 530 535 540	
10	ATC CTG AAC AAA GGC CAT GAC ATT TCA GCC GAC TAC TGG TCA CTG GGA	1680
	Ile Leu Asn Lys Gly His Asp Ile Ser Ala Asp Tyr Trp Ser Leu Gly 545 550 555 560	
15	ATC CTA ATG TAT GAA CTC CTG ACT GGC AGC CCA CCT TTC TCA GGC CCA	1728
	Ile Leu Met Tyr Glu Leu Leu Thr Gly Ser Pro Pro Phe Ser Gly Pro 565 570 575	
20	GAT CCT ATG AAA ACC TAT AAC ATC ATA TTG AGG GGG ATT GAC ATG ATA	1776
	Asp Pro Met Lys Thr Tyr Asn Ile Ile Leu Arg Gly Ile Asp Met Ile 580 585 590	
25	GAA TTT CCA AAG AAG ATT GCC AAA AAT GCT GCT AAT TTA ATT AAA AAA	1824
	Glu Phe Pro Lys Lys Ile Ala Lys Asn Ala Ala Asn Leu Ile Lys Lys 595 600 605	
30	CTA TGC AGG GAC AAT CCA TCA GAA AGA TTA GGG AAT TTG AAA AAT GGA	1872
	Leu Cys Arg Asp Asn Pro Ser Glu Arg Leu Gly Asn Leu Lys Asn Gly 610 615 620	
35	GTA AAA GAC ATT CAA AAG CAC AAA TGG TTT GAG GGC TTT AAC TGG GAA	1920
	Val Lys Asp Ile Gln Lys His Lys Trp Phe Glu Gly Phe Asn Trp Glu 625 630 635 640	
40	GGC TTA AGA AAA GGT ACC TTG ACA CCT CCT ATA ATA CCA AGT GTT GCA	1968
	Gly Leu Arg Lys Gly Thr Leu Thr Pro Pro Ile Ile Pro Ser Val Ala 645 650 655	
45	TCA CCC ACA GAC ACA AGT AAT TTT GAC AGT TTC CCT GAG GAC AAC GAT	2016
	Ser Pro Thr Asp Thr Ser Asn Phe Asp Ser Phe Pro Glu Asp Asn Asp 660 665 670	
50	GAA CCA CCA CCT GAT GAC AAC TCA GGA TGG GAT ATA GAC TTC TCG GAT	2064
	Glu Pro Pro Pro Asp Asp Asn Ser Gly Trp Asp Ile Asp Phe Ser Asp 675 680 685	
55	CCA CCG GTC GCC ACC ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG	2112
	Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly 690 695 700	
60	GTG GTG CCC ATC CTG GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG	2160
	Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys 705 710 715 720	
65	TTC AGC GTG TCC GGC GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG	2208
	Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu 725 730 735	
70	ACC CTG AAG TTC ATC TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC	2256
	Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro 740 745 750	

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	ACC	CTC	GTG	ACC	ACC	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	2304
	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	
			755					760					765				
5	CCC	GAC	CAC	ATG	AAG	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	2352
	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	
		770					775					780					
10	GGC	TAC	GTC	CAG	GAG	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	2400
	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	
	785					790					795				800		
15	AAG	ACC	CGC	GCC	GAG	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	2448
	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	
				805						810					815		
20	ATC	GAG	CTG	AAG	GGC	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	2496
	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	
			820						825					830			
25	CAC	AAG	CTG	GAG	TAC	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	2544
	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	
			835					840					845				
30	GAC	AAG	CAG	AAG	AAC	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	2592
	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	
		850				855					860						
35	ATC	GAG	GAC	GGC	AGC	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	2640
	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	
	865					870				875					880		
40	CCC	ATC	GGC	GAC	GGC	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	2688
	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	
				885						890					895		
45	ACC	CAG	TCC	GCC	CTG	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	2736
	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	
			900						905					910			
50	GTC	CTG	CTG	GAG	TTC	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	2784
	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	
			915					920					925				
55	GAG	CTG	TAC	AA	GTAA												2799
	Glu	Leu	Tyr	Lys													
			930														

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 932 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

280

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

	Met	Gly	Thr	Leu	Arg	Asp	Leu	Gln	Tyr	Ala	Leu	Gln	Glu	Lys	Ile	Glu	
	1				5					10					15		
10	Glu	Leu	Arg	Gln	Arg	Asp	Ala	Leu	Ile	Asp	Glu	Leu	Glu	Leu	Glu	Leu	
				20					25					30			
	Asp	Gln	Lys	Asp	Glu	Leu	Ile	Gln	Lys	Leu	Gln	Asn	Glu	Leu	Asp	Lys	
			35					40					45				
15	Tyr	Arg	Ser	Val	Ile	Arg	Pro	Ala	Thr	Gln	Gln	Ala	Gln	Lys	Gln	Ser	
		50					55					60					
	Ala	Ser	Thr	Leu	Gln	Gly	Glu	Pro	Arg	Thr	Lys	Arg	Gln	Ala	Ile	Ser	
	65					70					75				80		
	Ala	Glu	Pro	Thr	Ala	Phe	Asp	Ile	Gln	Asp	Leu	Ser	His	Val	Thr	Leu	
					85				90						95		
20	Pro	Phe	Tyr	Pro	Lys	Ser	Pro	Gln	Ser	Lys	Asp	Leu	Ile	Lys	Glu	Ala	
				100					105					110			
	Ile	Leu	Asp	Asn	Asp	Phe	Met	Lys	Asn	Leu	Glu	Leu	Ser	Gln	Ile	Gln	
			115					120					125				
25	Glu	Ile	Val	Asp	Cys	Met	Tyr	Pro	Val	Glu	Tyr	Gly	Lys	Asp	Ser	Cys	
		130					135					140					
	Ile	Ile	Lys	Glu	Gly	Asp	Val	Gly	Ser	Leu	Val	Tyr	Val	Met	Glu	Asp	
	145					150					155				160		
	Gly	Lys	Val	Glu	Val	Thr	Lys	Glu	Gly	Val	Lys	Leu	Cys	Thr	Met	Gly	
					165				170						175		
30	Pro	Gly	Lys	Val	Phe	Gly	Glu	Leu	Ala	Ile	Leu	Tyr	Asn	Cys	Thr	Arg	
				180					185					190			
	Thr	Ala	Thr	Val	Lys	Thr	Leu	Val	Asn	Val	Lys	Leu	Trp	Ala	Ile	Asp	
			195				200						205				
35	Arg	Gln	Cys	Phe	Gln	Thr	Ile	Met	Met	Arg	Thr	Gly	Leu	Ile	Lys	His	
		210				215						220					
	Thr	Glu	Tyr	Met	Glu	Phe	Leu	Lys	Ser	Val	Pro	Thr	Phe	Gln	Ser	Leu	
	225					230					235				240		
	Pro	Glu	Glu	Ile	Leu	Ser	Lys	Leu	Ala	Asp	Val	Leu	Glu	Glu	Thr	His	
					245				250						255		
40	Tyr	Glu	Asn	Gly	Glu	Tyr	Ile	Ile	Arg	Gln	Gly	Ala	Arg	Gly	Asp	Thr	
				260					265					270			
	Phe	Phe	Ile	Ile	Ser	Lys	Gly	Thr	Val	Asn	Val	Thr	Arg	Glu	Asp	Ser	
			275				280						285				
45	Pro	Ser	Glu	Asp	Pro	Val	Phe	Leu	Arg	Thr	Leu	Gly	Lys	Gly	Asp	Trp	
		290				295					300						
	Phe	Gly	Glu	Lys	Ala	Leu	Gln	Gly	Glu	Asp	Val	Arg	Thr	Ala	Asn	Val	
	305					310					315				320		
	Ile	Ala	Ala	Glu	Ala	Val	Thr	Cys	Leu	Val	Ile	Asp	Arg	Asp	Ser	Phe	
					325				330						335		
50	Lys	His	Leu	Ile	Gly	Gly	Leu	Asp	Asp	Val	Ser	Asn	Lys	Ala	Tyr	Glu	
				340					345					350			
	Asp	Ala	Glu	Ala	Lys	Ala	Lys	Tyr	Glu	Ala	Glu	Ala	Ala	Phe	Phe	Ala	
			355				360						365				
55	Asn	Leu	Lys	Leu	Ser	Asp	Phe	Asn	Ile	Ile	Asp	Thr	Leu	Gly	Val	Gly	
		370				375					380						
	Gly	Phe	Gly	Arg	Val	Glu	Leu	Val	Gln	Leu	Lys	Ser	Glu	Glu	Ser	Lys	

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[illegible]

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835 840 845  
 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn  
 850 855 860  
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr  
 5 865 870 875 880  
 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser  
 885 890 895  
 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met  
 900 905 910  
 10 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp  
 915 920 925  
 Glu Leu Tyr Lys  
 930

15 (2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2184 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

25

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2181

(D) OTHER INFORMATION:

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
GTC GAG CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
GAG GGC GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
TGC ACC ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
CTG ACC TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG	240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
CAG CAC GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG	288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
CGC ACC ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG	336

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	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
5	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115					120					125				
10	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
			130				135					140					
15	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150				155					160		
	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165				170				175				
20	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180					185					190			
25	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195					200					205				
30	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210					215					220					
35	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720
	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225					230				235					240		
	GGA	CTC	AGA	TCT	CGA	GGC	ACC	ATG	AGC	GAC	GTG	GCT	ATT	GTG	AAG	GAG	768
	Gly	Leu	Arg	Ser	Arg	Gly	Thr	Met	Ser	Asp	Val	Ala	Ile	Val	Lys	Glu	
					245				250					255			
40	GGT	TGG	CTG	CAC	AAA	CGA	GGG	GAG	TAC	ATC	AAG	ACC	TGG	CGG	CCA	CGC	816
	Gly	Trp	Leu	His	Lys	Arg	Gly	Glu	Tyr	Ile	Lys	Thr	Trp	Arg	Pro	Arg	
				260				265						270			
45	TAC	TTC	CTC	CTC	AAG	AAT	GAT	GGC	ACC	TTC	ATT	GGC	TAC	AAG	GAG	CGG	864
	Tyr	Phe	Leu	Leu	Lys	Asn	Asp	Gly	Thr	Phe	Ile	Gly	Tyr	Lys	Glu	Arg	
			275					280					285				
50	CCG	CAG	GAT	GTG	GAC	CAA	CGT	GAG	GCT	CCC	CTC	AAC	AAC	TTC	TCT	GTG	912
	Pro	Gln	Asp	Val	Asp	Gln	Arg	Glu	Ala	Pro	Leu	Asn	Asn	Phe	Ser	Val	
		290					295					300					
55	GCG	CAG	TGC	CAG	CTG	ATG	AAG	ACG	GAG	CGG	CCC	CGG	CCC	AAC	ACC	TTC	960
	Ala	Gln	Cys	Gln	Leu	Met	Lys	Thr	Glu	Arg	Pro	Arg	Pro	Asn	Thr	Phe	
	305					310				315				320			
	ATC	ATC	CGC	TGC	CTG	CAG	TGG	ACC	ACT	GTC	ATC	GAA	CGC	ACC	TTC	CAT	1008

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	Ile	Ile	Arg	Cys	Leu	Gln	Trp	Thr	Thr	Val	Ile	Glu	Arg	Thr	Phe	His	
					325					330					335		
5	GTG	GAG	ACT	CCT	GAG	GAG	CGG	GAG	GAG	TGG	ACA	ACC	GCC	ATC	CAG	ACT	1056
	Val	Glu	Thr	Pro	Glu	Glu	Arg	Glu	Glu	Trp	Thr	Thr	Ala	Ile	Gln	Thr	
				340				345						350			
10	GTG	GCT	GAC	GGC	CTC	AAG	AAG	CAG	GAG	GAG	GAG	GAG	ATG	GAC	TTC	CGG	1104
	Val	Ala	Asp	Gly	Leu	Lys	Lys	Gln	Glu	Glu	Glu	Glu	Met	Asp	Phe	Arg	
			355					360						365			
15	TCG	GGC	TCA	CCC	AGT	GAC	AAC	TCA	GGG	GCT	GAA	GAG	ATG	GAG	GTG	TCC	1152
	Ser	Gly	Ser	Pro	Ser	Asp	Asn	Ser	Gly	Ala	Glu	Glu	Met	Glu	Val	Ser	
		370					375						380				
20	CTG	GCC	AAG	CCC	AAG	CAC	CGC	GTG	ACC	ATG	AAC	GAG	TTT	GAG	TAC	CTG	1200
	Leu	Ala	Lys	Pro	Lys	His	Arg	Val	Thr	Met	Asn	Glu	Phe	Glu	Tyr	Leu	
		385				390					395					400	
25	AAG	CTG	CTG	GGC	AAG	GGC	ACT	TTC	GGC	AAG	GTG	ATC	CTG	GTG	AAG	GAG	1248
	Lys	Leu	Leu	Gly	Lys	Gly	Thr	Phe	Gly	Lys	Val	Ile	Leu	Val	Lys	Glu	
				405					410						415		
30	AAG	GCC	ACA	GGC	CGC	TAC	TAC	GCC	ATG	AAG	ATC	CTC	AAG	AAG	GAA	GTC	1296
	Lys	Ala	Thr	Gly	Arg	Tyr	Tyr	Ala	Met	Lys	Ile	Leu	Lys	Lys	Glu	Val	
				420					425						430		
35	ATC	GTG	GCC	AAG	GAC	GAG	GTG	GCC	CAC	ACA	CTC	ACC	GAG	AAC	CGC	GTC	1344
	Ile	Val	Ala	Lys	Asp	Glu	Val	Ala	His	Thr	Leu	Thr	Glu	Asn	Arg	Val	
			435					440							445		
40	CTG	CAG	AAC	TCC	AGG	CAC	CCC	TTC	CTC	ACA	GCC	CTG	AAG	TAC	TCT	TTC	1392
	Leu	Gln	Asn	Ser	Arg	His	Pro	Phe	Leu	Thr	Ala	Leu	Lys	Tyr	Ser	Phe	
			450				455						460				
45	CAG	ACC	CAC	GAC	CGC	CTC	TGC	TTT	GTC	ATG	GAG	TAC	GCC	AAC	GGG	GGC	1440
	Gln	Thr	His	Asp	Arg	Leu	Cys	Phe	Val	Met	Glu	Tyr	Ala	Asn	Gly	Gly	
		465				470				475					480		
50	GAG	CTG	TTC	TTC	CAC	CTG	TCC	CGG	GAA	CGT	GTG	TTC	TCC	GAG	GAC	CGG	1488
	Glu	Leu	Phe	Phe	His	Leu	Ser	Arg	Glu	Arg	Val	Phe	Ser	Glu	Asp	Arg	
					485				490						495		
55	GCC	CGC	TTC	TAT	GGC	GCT	GAG	ATT	GTG	TCA	GCC	CTG	GAC	TAC	CTG	CAC	1536
	Ala	Arg	Phe	Tyr	Gly	Ala	Glu	Ile	Val	Ser	Ala	Leu	Asp	Tyr	Leu	His	
			500					505						510			
60	TCG	GAG	AAG	AAC	GTG	GTG	TAC	CGG	GAC	CTC	AAG	CTG	GAG	AAC	CTC	ATG	1584
	Ser	Glu	Lys	Asn	Val	Val	Tyr	Arg	Asp	Leu	Lys	Leu	Glu	Asn	Leu	Met	
			515					520						525			
65	CTG	GAC	AAG	GAC	GGG	CAC	ATT	AAG	ATC	ACA	GAC	TTC	GGG	CTG	TGC	AAG	1632
	Leu	Asp	Lys	Asp	Gly	His	Ile	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Cys	Lys	
		530					535						540				
70	GAG	GGG	ATC	AAG	GAC	GGT	GCC	ACC	ATG	AAG	ACC	TTT	TGC	GGC	ACA	CCT	1680

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	Glu	Gly	Ile	Lys	Asp	Gly	Ala	Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro	
	545					550					555					560	
5	GAG	TAC	CTG	GCC	CCC	GAG	GTG	CTG	GAG	GAC	AAT	GAC	TAC	GGC	CGT	GCA	1728
	Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala	
					565					570					575		
10	GTG	GAC	TGG	TGG	GGG	CTG	GGC	GTG	GTC	ATG	TAC	GAG	ATG	ATG	TGC	GGT	1776
	Val	Asp	Trp	Trp	Gly	Leu	Gly	Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly	
				580					585					590			
15	CGC	CTG	CCC	TTC	TAC	AAC	CAG	GAC	CAT	GAG	AAG	CTT	TTT	GAG	CTC	ATC	1824
	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	Asp	His	Glu	Lys	Leu	Phe	Glu	Leu	Ile	
			595				600						605				
	CTC	ATG	GAG	GAG	ATC	CGC	TTC	CCG	CGC	ACG	CTT	GGT	CCC	GAG	GCC	AAG	1872
	Leu	Met	Glu	Glu	Ile	Arg	Phe	Pro	Arg	Thr	Leu	Gly	Pro	Glu	Ala	Lys	
	610						615					620					
20	TCC	TTG	CTT	TCA	GGG	CTG	CTC	AAG	AAG	GAC	CCC	AAG	CAG	AGG	CTT	GGC	1920
	Ser	Leu	Leu	Ser	Gly	Leu	Leu	Lys	Lys	Asp	Pro	Lys	Gln	Arg	Leu	Gly	
	625					630					635					640	
25	GGG	GGC	TCC	GAG	GAC	GCC	AAG	GAG	ATC	ATG	CAG	CAT	CGC	TTC	TTT	GCC	1968
	Gly	Gly	Ser	Glu	Asp	Ala	Lys	Glu	Ile	Met	Gln	His	Arg	Phe	Phe	Ala	
					645					650					655		
30	GGT	ATC	GTG	TGG	CAG	CAC	GTG	TAC	GAG	AAG	AAG	CTC	AGC	CCA	CCC	TTC	2016
	Gly	Ile	Val	Trp	Gln	His	Val	Tyr	Glu	Lys	Lys	Leu	Ser	Pro	Pro	Phe	
				660					665					670			
35	AAG	CCC	CAG	GTC	ACG	TCG	GAG	ACT	GAC	ACC	AGG	TAT	TTT	GAT	GAG	GAG	2064
	Lys	Pro	Gln	Val	Thr	Ser	Glu	Thr	Asp	Thr	Arg	Tyr	Phe	Asp	Glu	Glu	
			675					680					685				
	TTC	ACG	GCC	CAG	ATG	ATC	ACC	ATC	ACA	CCA	CCT	GAC	CAA	GAT	GAC	AGC	2112
	Phe	Thr	Ala	Gln	Met	Ile	Thr	Ile	Thr	Pro	Pro	Asp	Gln	Asp	Asp	Ser	
	690						695					700					
40	ATG	GAG	TGT	GTG	GAC	AGC	GAG	CGC	AGG	CCC	CAC	TTC	CCC	CAG	TTC	TCC	2160
	Met	Glu	Cys	Val	Asp	Ser	Glu	Arg	Arg	Pro	His	Phe	Pro	Gln	Phe	Ser	
	705					710				715						720	
45	TAC	TCG	GCC	AGC	AGC	ACG	GCC	TGA									2184
	Tyr	Ser	Ala	Ser	Ser	Thr	Ala										
					725												

(2) INFORMATION FOR SEQ ID NO:139:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

55

(D) TOPOLOGY: linear

286

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(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

5  
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
1 5 10 15  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
10 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
15 65 70 75 80  
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
20 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125  
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140  
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
25 145 150 155 160  
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
165 170 175  
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190  
30 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
195 200 205  
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220  
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser  
35 225 230 235 240  
Gly Leu Arg Ser Arg Gly Thr Met Ser Asp Val Ala Ile Val Lys Glu  
245 250 255  
Gly Trp Leu His Lys Arg Gly Glu Tyr Ile Lys Thr Trp Arg Pro Arg  
260 265 270  
40 Tyr Phe Leu Leu Lys Asn Asp Gly Thr Phe Ile Gly Tyr Lys Glu Arg  
275 280 285  
Pro Gln Asp Val Asp Gln Arg Glu Ala Pro Leu Asn Asn Phe Ser Val  
290 295 300  
Ala Gln Cys Gln Leu Met Lys Thr Glu Arg Pro Arg Pro Asn Thr Phe  
45 305 310 315 320  
Ile Ile Arg Cys Leu Gln Trp Thr Thr Val Ile Glu Arg Thr Phe His  
325 330 335  
Val Glu Thr Pro Glu Glu Arg Glu Glu Trp Thr Thr Ala Ile Gln Thr  
340 345 350  
50 Val Ala Asp Gly Leu Lys Lys Gln Glu Glu Glu Glu Met Asp Phe Arg  
355 360 365  
Ser Gly Ser Pro Ser Asp Asn Ser Gly Ala Glu Glu Met Glu Val Ser  
370 375 380  
Leu Ala Lys Pro Lys His Arg Val Thr Met Asn Glu Phe Glu Tyr Leu  
55 385 390 395 400  
Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile Leu Val Lys Glu

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405 410 415  
 Lys Ala Thr Gly Arg Tyr Tyr Ala Met Lys Ile Leu Lys Lys Glu Val  
 420 425 430  
 5 Ile Val Ala Lys Asp Glu Val Ala His Thr Leu Thr Glu Asn Arg Val  
 435 440 445  
 Leu Gln Asn Ser Arg His Pro Phe Leu Thr Ala Leu Lys Tyr Ser Phe  
 450 455 460  
 Gln Thr His Asp Arg Leu Cys Phe Val Met Glu Tyr Ala Asn Gly Gly  
 465 470 475 480  
 10 Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe Ser Glu Asp Arg  
 485 490 495  
 Ala Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu Asp Tyr Leu His  
 500 505 510  
 Ser Glu Lys Asn Val Val Tyr Arg Asp Leu Lys Leu Glu Asn Leu Met  
 15 515 520 525  
 Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly Leu Cys Lys  
 530 535 540  
 Glu Gly Ile Lys Asp Gly Ala Thr Met Lys Thr Phe Cys Gly Thr Pro  
 545 550 555 560  
 20 Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr Gly Arg Ala  
 565 570 575  
 Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met Met Cys Gly  
 580 585 590  
 Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys Leu Phe Glu Leu Ile  
 25 595 600 605  
 Leu Met Glu Glu Ile Arg Phe Pro Arg Thr Leu Gly Pro Glu Ala Lys  
 610 615 620  
 Ser Leu Leu Ser Gly Leu Leu Lys Lys Asp Pro Lys Gln Arg Leu Gly  
 625 630 635 640  
 30 Gly Gly Ser Glu Asp Ala Lys Glu Ile Met Gln His Arg Phe Phe Ala  
 645 650 655  
 Gly Ile Val Trp Gln His Val Tyr Glu Lys Lys Leu Ser Pro Pro Phe  
 660 665 670  
 Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu  
 35 675 680 685  
 Phe Thr Ala Gln Met Ile Thr Ile Thr Pro Pro Asp Gln Asp Asp Ser  
 690 695 700  
 Met Glu Cys Val Asp Ser Glu Arg Arg Pro His Phe Pro Gln Phe Ser  
 705 710 715 720  
 40 Tyr Ser Ala Ser Ser Thr Ala  
 725

## (2) INFORMATION FOR SEQ ID NO:140:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2394 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 50  
 (ii) MOLECULE TYPE: cDNA  
 (ix) FEATURE:  
 (A) NAME/KEY: Coding Sequence  
 55 (B) LOCATION: 1...2391  
 (D) OTHER INFORMATION:

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

5	ATG GAC GAA CTG TTC CCC CTC ATC TTC CCG GCA GAG CCA GCC CAG GCC	48
	Met Asp Glu Leu Phe Pro Leu Ile Phe Pro Ala Glu Pro Ala Gln Ala	
	1 5 10 15	
10	TCT GGC CCC TAT GTG GAG ATC ATT GAG CAG CCC AAG CAG CGG GGC ATG	96
	Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met	
	20 25 30	
15	CGC TTC CGC TAC AAG TGC GAG GGG CGC TCC GCG GGC AGC ATC CCA GGC	144
	Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly	
	35 40 45	
20	GAG AGG AGC ACA GAT ACC ACC AAG ACC CAC CCC ACC ATC AAG ATC AAT	192
	Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn	
	50 55 60	
25	GGC TAC ACA GGA CCA GGG ACA GTG CGC ATC TCC CTG GTC ACC AAG GAC	240
	Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp	
	65 70 75 80	
30	CCT CCT CAC CGG CCT CAC CCC CAC GAG CTT GTA GGA AAG GAC TGC CGG	288
	Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg	
	85 90 95	
35	GAT GGC TTC TAT GAG GCT GAG CTC TGC CCG GAC CGC TGC ATC CAC AGT	336
	Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser	
	100 105 110	
40	TTC CAG AAC CTG GGA ATC CAG TGT GTG AAG AAG CGG GAC CTG GAG CAG	384
	Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln	
	115 120 125	
45	GCT ATC AGT CAG CGC ATC CAG ACC AAC AAC AAC CCC TTC CAA GTT CCT	432
	Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro	
	130 135 140	
50	ATA GAA GAG CAG CGT GGG GAC TAC GAC CTG AAT GCT GTG CGG CTC TGC	480
	Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys	
	145 150 155 160	
55	TTC CAG GTG ACA GTG CGG GAC CCA TCA GGC AGG CCC CTC CGC CTG CCG	528
	Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro	
	165 170 175	
60	CCT GTC CTT CCT CAT CCC ATC TTT GAC AAT CGT GCC CCC AAC ACT GCC	576
	Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala	
	180 185 190	
65	GAG CTC AAG ATC TGC CGA GTG AAC CGA AAC TCT GGC AGC TGC CTC GGT	624
	Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly	
	195 200 205	
70	GGG GAT GAG ATC TTC CTA CTG TGT GAC AAG GTG CAG AAA GAG GAC ATT	672

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	Gly	Asp	Glu	Ile	Phe	Leu	Leu	Cys	Asp	Lys	Val	Gln	Lys	Glu	Asp	Ile	
	210						215					220					
5	GAG	GTG	TAT	TTC	ACG	GGA	CCA	GGC	TGG	GAG	GCC	CGA	GGC	TCC	TTT	TCG	720
	Glu	Val	Tyr	Phe	Thr	Gly	Pro	Gly	Trp	Glu	Ala	Arg	Gly	Ser	Phe	Ser	
	225					230				235						240	
10	CAA	GCT	GAT	GTG	CAC	CGA	CAA	GTG	GCC	ATT	GTG	TTC	CGG	ACC	CCT	CCC	768
	Gln	Ala	Asp	Val	His	Arg	Gln	Val	Ala	Ile	Val	Phe	Arg	Thr	Pro	Pro	
					245				250						255		
15	TAC	GCA	GAC	CCC	AGC	CTG	CAG	GCT	CCT	GTG	CGT	GTC	TCC	ATG	CAG	CTG	816
	Tyr	Ala	Asp	Pro	Ser	Leu	Gln	Ala	Pro	Val	Arg	Val	Ser	Met	Gln	Leu	
				260					265					270			
20	CGG	CGG	CCT	TCC	GAC	CGG	GAG	CTC	AGT	GAG	CCC	ATG	GAA	TTC	CAG	TAC	864
	Arg	Arg	Pro	Ser	Asp	Arg	Glu	Leu	Ser	Glu	Pro	Met	Glu	Phe	Gln	Tyr	
			275					280					285				
25	CTG	CCA	GAT	ACA	GAC	GAT	CGT	CAC	CGG	ATT	GAG	GAG	AAA	CGT	AAA	AGG	912
	Leu	Pro	Asp	Thr	Asp	Asp	Arg	His	Arg	Ile	Glu	Glu	Lys	Arg	Lys	Arg	
		290					295						300				
30	ACA	TAT	GAG	ACC	TTC	AAG	AGC	ATC	ATG	AAG	AAG	AGT	CCT	TTC	AGC	GGA	960
	Thr	Tyr	Glu	Thr	Phe	Lys	Ser	Ile	Met	Lys	Lys	Ser	Pro	Phe	Ser	Gly	
	305					310					315					320	
35	CCC	ACC	GAC	CCC	CGG	CCT	CCA	CCT	CGA	CGC	ATT	GCT	GTG	CCT	TCC	CGC	1008
	Pro	Thr	Asp	Pro	Arg	Pro	Pro	Pro	Arg	Arg	Ile	Ala	Val	Pro	Ser	Arg	
					325					330					335		
40	AGC	TCA	GCT	TCT	GTC	CCC	AAG	CCA	GCA	CCC	CAG	CCC	TAT	CCC	TTT	ACG	1056
	Ser	Ser	Ala	Ser	Val	Pro	Lys	Pro	Ala	Pro	Gln	Pro	Tyr	Pro	Phe	Thr	
				340					345				350				
45	TCA	TCC	CTG	AGC	ACC	ATC	AAC	TAT	GAT	GAG	TTT	CCC	ACC	ATG	GTG	TTT	1104
	Ser	Ser	Leu	Ser	Thr	Ile	Asn	Tyr	Asp	Glu	Phe	Pro	Thr	Met	Val	Phe	
			355				360						365				
50	CCT	TCT	GGG	CAG	ATC	AGC	CAG	GCC	TCG	GCC	TTG	GCC	CCG	GCC	CCT	CCC	1152
	Pro	Ser	Gly	Gln	Ile	Ser	Gln	Ala	Ser	Ala	Leu	Ala	Pro	Ala	Pro	Pro	
		370					375					380					
55	CAA	GTC	CTG	CCC	CAG	GCT	CCA	GCC	CCT	GCC	CCT	GCT	CCA	GCC	ATG	GTA	1200
	Gln	Val	Leu	Pro	Gln	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Met	Val	
	385					390				395					400		
60	TCA	GCT	CTG	GCC	CAG	GCC	CCA	GCC	CCT	GTC	CCA	GTC	CTA	GCC	CCA	GGC	1248
	Ser	Ala	Leu	Ala	Gln	Ala	Pro	Ala	Pro	Val	Pro	Val	Leu	Ala	Pro	Gly	
				405					410						415		
65	CCT	CCT	CAG	GCT	GTG	GCC	CCA	CCT	GCC	CCC	AAG	CCC	ACC	CAG	GCT	GGG	1296
	Pro	Pro	Gln	Ala	Val	Ala	Pro	Pro	Ala	Pro	Lys	Pro	Thr	Gln	Ala	Gly	
				420					425					430			
70	GAA	GGA	ACG	CTG	TCA	GAG	GCC	CTG	CTG	CAG	CTG	CAG	TTT	GAT	GAT	GAA	1344

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	Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu	
	435 440 445	
5	GAC CTG GGG GCC TTG CTT GGC AAC AGC ACA GAC CCA GCT GTG TTC ACA Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr	1392
	450 455 460	
10	GAC CTG GCA TCC GTC GAC AAC TCC GAG TTT CAG CAG CTG CTG AAC CAG Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln	1440
	465 470 475 480	
15	GGC ATA CCT GTG GCC CCC CAC ACA ACT GAG CCC ATG CTG ATG GAG TAC Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr	1488
	485 490 495	
	CCT GAG GCT ATA ACT CGC CTA GTG ACA GGG GCC CAG AGG CCC CCC GAC Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp	1536
	500 505 510	
20	CCA GCT CCT GCT CCA CTG GGG GCC CCG GGG CTC CCC AAT GGC CTC CTT Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu	1584
	515 520 525	
25	TCA GGA GAT GAA GAC TTC TCC TCC ATT GCG GAC ATG GAC TTC TCA GCC Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala	1632
	530 535 540	
30	CTG CTG AGT CAG ATC AGC TCC TTG GAT CCA CCG GTC GCC ACC ATG GTG Leu Leu Ser Gln Ile Ser Ser Leu Asp Pro Pro Val Ala Thr Met Val	1680
	545 550 555 560	
35	AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG GTC GAG Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu	1728
	565 570 575	
	CTG GAC GGC GAC GTA AAC GGC CAC AAG TTC AGC GTG TCC GGC GAG GGC Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly	1776
	580 585 590	
40	GAG GGC GAT GCC ACC TAC GGC AAG CTG ACC CTG AAG TTC ATC TGC ACC Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr	1824
	595 600 605	
45	ACC GGC AAG CTG CCC GTG CCC TGG CCC ACC CTC GTG ACC ACC CTG ACC Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr	1872
	610 615 620	
50	TAC GGC GTG CAG TGC TTC AGC CGC TAC CCC GAC CAC ATG AAG CAG CAC Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His	1920
	625 630 635 640	
55	GAC TTC TTC AAG TCC GCC ATG CCC GAA GGC TAC GTC CAG GAG CGC ACC Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr	1968
	645 650 655	
	ATC TTC TTC AAG GAC GAC GGC AAC TAC AAG ACC CGC GCC GAG GTG AAG	2016

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	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	
				660					665						670		
5	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	ATC	GAC	2064
	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	
			675					680					685				
10	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	AAC	TAC	2112
	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	
			690				695					700					
15	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	GGC	ATC	2160
	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	
						710					715				720		
	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	GTG	CAG	2208
	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	
					725					730				735			
20	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	CCC	GTG	2256
	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	
				740					745					750			
25	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	AGC	AAA	2304
	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	
			755					760					765				
30	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	GTG	ACC	2352
	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	
			770				775					780					
35	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TAA			2394
	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys				
			785			790					795						

## (2) INFORMATION FOR SEQ ID NO:141:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 797 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

50	Met	Asp	Glu	Leu	Phe	Pro	Leu	Ile	Phe	Pro	Ala	Glu	Pro	Ala	Gln	Ala
	1				5				10					15		
	Ser	Gly	Pro	Tyr	Val	Glu	Ile	Ile	Glu	Gln	Pro	Lys	Gln	Arg	Gly	Met
				20				25					30			
	Arg	Phe	Arg	Tyr	Lys	Cys	Glu	Gly	Arg	Ser	Ala	Gly	Ser	Ile	Pro	Gly
55			35				40					45				
	Glu	Arg	Ser	Thr	Asp	Thr	Thr	Lys	Thr	His	Pro	Thr	Ile	Lys	Ile	Asn



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		50						55					60					
		Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp																
		65						70					75					80
5		Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg																
					85						90						95	
		Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser																
				100						105						110		
		Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln																
				115				120							125			
10		Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro																
				130				135						140				
		Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys																
		145				150						155						160
		Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro																
15				165						170							175	
		Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala																
				180						185						190		
		Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly																
				195				200							205			
20		Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile																
				210				215						220				
		Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser																
		225				230						235						240
		Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro																
25				245						250							255	
		Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met Gln Leu																
				260						265						270		
		Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe Gln Tyr																
				275				280							285			
30		Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg																
				290				295						300				
		Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly																
		305				310							315					320
		Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile Ala Val Pro Ser Arg																
35				325						330							335	
		Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe Thr																
				340						345						350		
		Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe Pro Thr Met Val Phe																
				355				360							365			
40		Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro Pro																
				370				375						380				
		Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Met Val																

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		500		505		510	
	Pro	Ala	Pro	Ala	Pro	Leu	Gly
		515		520		525	
5	Ser	Gly	Asp	Glu	Asp	Phe	Ser
		530		535		540	
	Leu	Leu	Ser	Gln	Ile	Ser	Ser
		545		550		555	
	Ser	Lys	Gly	Glu	Glu	Leu	Phe
				565		570	
10	Leu	Asp	Gly	Asp	Val	Asn	Gly
				580		585	
	Glu	Gly	Asp	Ala	Thr	Tyr	Gly
				595		600	
15	Thr	Gly	Lys	Leu	Pro	Val	Pro
				610		615	
	Tyr	Gly	Val	Gln	Cys	Phe	Ser
				625		630	
	Asp	Phe	Phe	Lys	Ser	Ala	Met
				645		650	
20	Ile	Phe	Phe	Lys	Asp	Asp	Gly
				660		665	
	Phe	Glu	Gly	Asp	Thr	Leu	Val
				675		680	
25	Phe	Lys	Glu	Asp	Gly	Asn	Ile
				690		695	
	Asn	Ser	His	Asn	Val	Tyr	Ile
				705		710	
	Lys	Val	Asn	Phe	Lys	Ile	Arg
				725		730	
30	Leu	Ala	Asp	His	Tyr	Gln	Gln
				740		745	
	Leu	Leu	Pro	Asp	Asn	His	Tyr
				755		760	
35	Asp	Pro	Asn	Glu	Lys	Arg	Asp
				770		775	
	Ala	Ala	Gly	Ile	Thr	Leu	Gly
				785		790	

## (2) INFORMATION FOR SEQ ID NO:142:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2394 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

45

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

50

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2391

(D) OTHER INFORMATION:

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ATG GTG AGC AAG GGC GAG GAG CTG TTC ACC GGG GTG GTG CCC ATC CTG

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	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
	1				5					10					15		
5	GTC	GAG	CTG	GAC	GGC	GAC	GTA	AAC	GGC	CAC	AAG	TTC	AGC	GTG	TCC	GGC	96
	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
				20					25					30			
10	GAG	GGC	GAG	GGC	GAT	GCC	ACC	TAC	GGC	AAG	CTG	ACC	CTG	AAG	TTC	ATC	144
	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
				35				40						45			
15	TGC	ACC	ACC	GGC	AAG	CTG	CCC	GTG	CCC	TGG	CCC	ACC	CTC	GTG	ACC	ACC	192
	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
				50			55					60					
20	CTG	ACC	TAC	GGC	GTG	CAG	TGC	TTC	AGC	CGC	TAC	CCC	GAC	CAC	ATG	AAG	240
	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65					70				75					80		
25	CAG	CAC	GAC	TTC	TTC	AAG	TCC	GCC	ATG	CCC	GAA	GGC	TAC	GTC	CAG	GAG	288
	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
					85					90					95		
30	CGC	ACC	ATC	TTC	TTC	AAG	GAC	GAC	GGC	AAC	TAC	AAG	ACC	CGC	GCC	GAG	336
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
				100					105					110			
35	GTG	AAG	TTC	GAG	GGC	GAC	ACC	CTG	GTG	AAC	CGC	ATC	GAG	CTG	AAG	GGC	384
	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
				115				120					125				
40	ATC	GAC	TTC	AAG	GAG	GAC	GGC	AAC	ATC	CTG	GGG	CAC	AAG	CTG	GAG	TAC	432
	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
				130			135					140					
45	AAC	TAC	AAC	AGC	CAC	AAC	GTC	TAT	ATC	ATG	GCC	GAC	AAG	CAG	AAG	AAC	480
	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145					150				155					160		
50	GGC	ATC	AAG	GTG	AAC	TTC	AAG	ATC	CGC	CAC	AAC	ATC	GAG	GAC	GGC	AGC	528
	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
					165				170						175		
55	GTG	CAG	CTC	GCC	GAC	CAC	TAC	CAG	CAG	AAC	ACC	CCC	ATC	GGC	GAC	GGC	576
	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
				180				185						190			
60	CCC	GTG	CTG	CTG	CCC	GAC	AAC	CAC	TAC	CTG	AGC	ACC	CAG	TCC	GCC	CTG	624
	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
				195				200						205			
65	AGC	AAA	GAC	CCC	AAC	GAG	AAG	CGC	GAT	CAC	ATG	GTC	CTG	CTG	GAG	TTC	672
	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
				210				215				220					
70	GTG	ACC	GCC	GCC	GGG	ATC	ACT	CTC	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TCC	720

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	Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
	225 230 235 240	
5	GGA CTC AGA TCT CGA GCC ATG GAC GAA CTG TTC CCC CTC ATC TTC CCG Gly Leu Arg Ser Arg Ala Met Asp Glu Leu Phe Pro Leu Ile Phe Pro	768
	245 250 255	
10	GCA GAG CCA GCC CAG GCC TCT GGC CCC TAT GTG GAG ATC ATT GAG CAG Ala Glu Pro Ala Gln Ala Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln	816
	260 265 270	
15	CCC AAG CAG CGG GGC ATG CGC TTC CGC TAC AAG TGC GAG GGG CGC TCC Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser	864
	275 280 285	
20	GCG GGC AGC ATC CCA GGC GAG AGG AGC ACA GAT ACC ACC AAG ACC CAC Ala Gly Ser Ile Pro Gly Glu Arg Ser Thr Asp Thr Thr Lys Thr His	912
	290 295 300	
25	CCC ACC ATC AAG ATC AAT GGC TAC ACA GGA CCA GGG ACA GTG CGC ATC Pro Thr Ile Lys Ile Asn Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile	960
	305 310 315 320	
30	TCC CTG GTC ACC AAG GAC CCT CCT CAC CGG CCT CAC CCC CAC GAG CTT Ser Leu Val Thr Lys Asp Pro Pro His Arg Pro His Pro His Glu Leu	1008
	325 330 335	
35	GTA GGA AAG GAC TGC CGG GAT GGC TTC TAT GAG GCT GAG CTC TGC CCG Val Gly Lys Asp Cys Arg Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro	1056
	340 345 350	
40	GAC CGC TGC ATC CAC AGT TTC CAG AAC CTG GGA ATC CAG TGT GTG AAG Asp Arg Cys Ile His Ser Phe Gln Asn Leu Gly Ile Gln Cys Val Lys	1104
	355 360 365	
45	AAG CGG GAC CTG GAG CAG GCT ATC AGT CAG CGC ATC CAG ACC AAC AAC Lys Arg Asp Leu Glu Gln Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn	1152
	370 375 380	
50	AAC CCC TTC CAA GTT CCT ATA GAA GAG CAG CGT GGG GAC TAC GAC CTG Asn Pro Phe Gln Val Pro Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu	1200
	385 390 395 400	
55	AAT GCT GTG CGG CTC TGC TTC CAG GTG ACA GTG CGG GAC CCA TCA GGC Asn Ala Val Arg Leu Cys Phe Gln Val Thr Val Arg Asp Pro Ser Gly	1248
	405 410 415	
60	AGG CCC CTC CGC CTG CCG CCT GTC CTT CCT CAT CCC ATC TTT GAC AAT Arg Pro Leu Leu Pro Pro Val Leu Pro His Pro Ile Phe Asp Asn	1296
	420 425 430	
65	CGT GCC CCC AAC ACT GCC GAG CTC AAG ATC TGC CGA GTG AAC CGA AAC Arg Ala Pro Asn Thr Ala Glu Leu Lys Ile Cys Arg Val Asn Arg Asn	1344
	435 440 445	
70	TCT GGC AGC TGC CTC GGT GGG GAT GAG ATC TTC CTA CTG TGT GAC AAG	1392

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	Ser Gly Ser Cys Leu Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys	
	450 455 460	
5	GTG CAG AAA GAG GAC ATT GAG GTG TAT TTC ACG GGA CCA GGC TGG GAG Val Gln Lys Glu Asp Ile Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu	1440
	465 470 475 480	
10	GCC CGA GGC TCC TTT TCG CAA GCT GAT GTG CAC CGA CAA GTG GCC ATT Ala Arg Gly Ser Phe Ser Gln Ala Asp Val His Arg Gln Val Ala Ile	1488
	485 490 495	
15	GTG TTC CGG ACC CCT CCC TAC GCA GAC CCC AGC CTG CAG GCT CCT GTG Val Phe Arg Thr Pro Pro Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val	1536
	500 505 510	
20	CGT GTC TCC ATG CAG CTG CGG CGG CCT TCC GAC CGG GAG CTC AGT GAG Arg Val Ser Met Gln Leu Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu	1584
	515 520 525	
25	CCC ATG GAA TTC CAG TAC CTG CCA GAT ACA GAC GAT CGT CAC CGG ATT Pro Met Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile	1632
	530 535 540	
30	GAG GAG AAA CGT AAA AGG ACA TAT GAG ACC TTC AAG AGC ATC ATG AAG Glu Glu Lys Arg Lys Arg Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys	1680
	545 550 555 560	
35	AAG AGT CCT TTC AGC GGA CCC ACC GAC CCC CGG CCT CCA CCT CGA CGC Lys Ser Pro Phe Ser Gly Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg	1728
	565 570 575	
40	ATT GCT GTG CCT TCC CGC AGC TCA GCT TCT GTC CCC AAG CCA GCA CCC Ile Ala Val Pro Ser Arg Ser Ser Ala Ser Val Pro Lys Pro Ala Pro	1776
	580 585 590	
45	CAG CCC TAT CCC TTT ACG TCA TCC CTG AGC ACC ATC AAC TAT GAT GAG Gln Pro Tyr Pro Phe Thr Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu	1824
	595 600 605	
50	TTT CCC ACC ATG GTG TTT CCT TCT GGG CAG ATC AGC CAG GCC TCG GCC Phe Pro Thr Met Val Phe Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala	1872
	610 615 620	
55	TTG GCC CCG GCC CCT CCC CAA GTC CTG CCC CAG GCT CCA GCC CCT GCC Leu Ala Pro Ala Pro Pro Gln Val Leu Pro Gln Ala Pro Ala Pro Ala	1920
	625 630 635 640	
60	CCT GCT CCA GCC ATG GTA TCA GCT CTG GCC CAG GCC CCA GCC CCT GTC Pro Ala Pro Ala Met Val Ser Ala Leu Ala Gln Ala Pro Ala Pro Val	1968
	645 650 655	
65	CCA GTC CTA GCC CCA GGC CCT CCT CAG GCT GTG GCC CCA CCT GCC CCC Pro Val Leu Ala Pro Gly Pro Pro Gln Ala Val Ala Pro Pro Ala Pro	2016
	660 665 670	
70	AAG CCC ACC CAG GCT GGG GAA GGA ACG CTG TCA GAG GCC CTG CTG CAG	2064

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	Lys	Pro	Thr	Gln	Ala	Gly	Glu	Gly	Thr	Leu	Ser	Glu	Ala	Leu	Leu	Gln	
			675					680					685				
5	CTG	CAG	TTT	GAT	GAT	GAA	GAC	CTG	GGG	GCC	TTG	CTT	GGC	AAC	AGC	ACA	2112
	Leu	Gln	Phe	Asp	Asp	Glu	Asp	Leu	Gly	Ala	Leu	Leu	Gly	Asn	Ser	Thr	
			690				695					700					
10	GAC	CCA	GCT	GTG	TTC	ACA	GAC	CTG	GCA	TCC	GTC	GAC	AAC	TCC	GAG	TTT	2160
	Asp	Pro	Ala	Val	Phe	Thr	Asp	Leu	Ala	Ser	Val	Asp	Asn	Ser	Glu	Phe	
			705			710					715					720	
15	CAG	CAG	CTG	CTG	AAC	CAG	GGC	ATA	CCT	GTG	GCC	CCC	CAC	ACA	ACT	GAG	2208
	Gln	Gln	Leu	Leu	Asn	Gln	Gly	Ile	Pro	Val	Ala	Pro	His	Thr	Thr	Glu	
					725					730					735		
	CCC	ATG	CTG	ATG	GAG	TAC	CCT	GAG	GCT	ATA	ACT	CGC	CTA	GTG	ACA	GGG	2256
	Pro	Met	Leu	Met	Glu	Tyr	Pro	Glu	Ala	Ile	Thr	Arg	Leu	Val	Thr	Gly	
				740					745					750			
20	GCC	CAG	AGG	CCC	CCC	GAC	CCA	GCT	CCT	GCT	CCA	CTG	GGG	GCC	CCG	GGG	2304
	Ala	Gln	Arg	Pro	Pro	Asp	Pro	Ala	Pro	Ala	Pro	Leu	Gly	Ala	Pro	Gly	
			755					760					765				
25	CTC	CCC	AAT	GGC	CTC	CTT	TCA	GGA	GAT	GAA	GAC	TTC	TCC	TCC	ATT	GCG	2352
	Leu	Pro	Asn	Gly	Leu	Leu	Ser	Gly	Asp	Glu	Asp	Phe	Ser	Ser	Ile	Ala	
			770				775					780					
30	GAC	ATG	GAC	TTC	TCA	GCC	CTG	CTG	AGT	CAG	ATC	AGC	TCC	TAA			2394
	Asp	Met	Asp	Phe	Ser	Ala	Leu	Leu	Ser	Gln	Ile	Ser	Ser				
			785			790					795						

## (2) INFORMATION FOR SEQ ID NO:143:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 797 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys

65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

298

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85 90 95  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 5 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
 10 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190  
 15 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
 195 200 205  
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220  
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser  
 225 230 235 240  
 20 Gly Leu Arg Ser Arg Ala Met Asp Glu Leu Phe Pro Leu Ile Phe Pro  
 245 250 255  
 Ala Glu Pro Ala Gln Ala Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln  
 260 265 270  
 25 Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser  
 275 280 285  
 Ala Gly Ser Ile Pro Gly Glu Arg Ser Thr Asp Thr Thr Lys Thr His  
 290 295 300  
 Pro Thr Ile Lys Ile Asn Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile  
 305 310 315 320  
 30 Ser Leu Val Thr Lys Asp Pro Pro His Arg Pro His Pro His Glu Leu  
 325 330 335  
 Val Gly Lys Asp Cys Arg Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro  
 340 345 350  
 35 Asp Arg Cys Ile His Ser Phe Gln Asn Leu Gly Ile Gln Cys Val Lys  
 355 360 365  
 Lys Arg Asp Leu Glu Gln Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn  
 370 375 380  
 Asn Pro Phe Gln Val Pro Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu  
 385 390 395 400  
 40 Asn Ala Val Arg Leu Cys Phe Gln Val Thr Val Arg Asp Pro Ser Gly  
 405 410 415  
 Arg Pro Leu Arg Leu Pro Pro Val Leu Pro His Pro Ile Phe Asp Asn  
 420 425 430  
 45 Arg Ala Pro Asn Thr Ala Glu Leu Lys Ile Cys Arg Val Asn Arg Asn  
 435 440 445  
 Ser Gly Ser Cys Leu Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys  
 450 455 460  
 Val Gln Lys Glu Asp Ile Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu  
 465 470 475 480  
 50 Ala Arg Gly Ser Phe Ser Gln Ala Asp Val His Arg Gln Val Ala Ile  
 485 490 495  
 Val Phe Arg Thr Pro Pro Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val  
 500 505 510  
 Arg Val Ser Met Gln Leu Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu  
 515 520 525  
 55 Pro Met Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile

299

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	530		535		540														
	Glu	Glu	Lys	Arg	Lys	Arg	Thr	Tyr	Glu	Thr	Phe	Lys	Ser	Ile	Met	Lys			
	545					550					555					560			
5	Lys	Ser	Pro	Phe	Ser	Gly	Pro	Thr	Asp	Pro	Arg	Pro	Pro	Pro	Arg	Arg			
					565					570						575			
	Ile	Ala	Val	Pro	Ser	Arg	Ser	Ser	Ala	Ser	Val	Pro	Lys	Pro	Ala	Pro			
				580					585					590					
	Gln	Pro	Tyr	Pro	Phe	Thr	Ser	Ser	Leu	Ser	Thr	Ile	Asn	Tyr	Asp	Glu			
		595						600					605						
10	Phe	Pro	Thr	Met	Val	Phe	Pro	Ser	Gly	Gln	Ile	Ser	Gln	Ala	Ser	Ala			
	610					615						620							
	Leu	Ala	Pro	Ala	Pro	Pro	Gln	Val	Leu	Pro	Gln	Ala	Pro	Ala	Pro	Ala			
	625					630					635					640			
	Pro	Ala	Pro	Ala	Met	Val	Ser	Ala	Leu	Ala	Gln	Ala	Pro	Ala	Pro	Val			
15					645					650						655			
	Pro	Val	Leu	Ala	Pro	Gly	Pro	Pro	Gln	Ala	Val	Ala	Pro	Pro	Ala	Pro			
				660					665					670					
	Lys	Pro	Thr	Gln	Ala	Gly	Glu	Gly	Thr	Leu	Ser	Glu	Ala	Leu	Leu	Gln			
		675						680					685						
20	Leu	Gln	Phe	Asp	Asp	Glu	Asp	Leu	Gly	Ala	Leu	Leu	Gly	Asn	Ser	Thr			
	690					695						700							
	Asp	Pro	Ala	Val	Phe	Thr	Asp	Leu	Ala	Ser	Val	Asp	Asn	Ser	Glu	Phe			
	705					710					715					720			
	Gln	Gln	Leu	Leu	Asn	Gln	Gly	Ile	Pro	Val	Ala	Pro	His	Thr	Thr	Glu			
25					725					730						735			
	Pro	Met	Leu	Met	Glu	Tyr	Pro	Glu	Ala	Ile	Thr	Arg	Leu	Val	Thr	Gly			
				740					745					750					
	Ala	Gln	Arg	Pro	Pro	Asp	Pro	Ala	Pro	Ala	Pro	Leu	Gly	Ala	Pro	Gly			
		755						760					765						
30	Leu	Pro	Asn	Gly	Leu	Leu	Ser	Gly	Asp	Glu	Asp	Phe	Ser	Ser	Ile	Ala			
	770					775						780							
	Asp	Met	Asp	Phe	Ser	Ala	Leu	Leu	Ser	Gln	Ile	Ser	Ser						
	785					790					795								

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